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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:19:38 ; Search time 27.5 Seconds  
(without alignments)  
21.704 Million cell updates/sec

Title: US-10-042-202-1  
Perfect score: 48  
Sequence: 1 HLGNVKYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	4	US-09-454-204A-20
2	48	100.0	229	4	US-09-454-204A-41
3	48	100.0	559	1	US-08-313-288B-14
4	40	83.3	15	4	US-09-009-953-44
5	39	81.2	133	1	US-07-846-992-3
6	39	81.2	133	1	US-08-469-555-3
7	37	77.1	285	4	US-09-328-352-7616
8	36	75.0	376	4	US-09-248-796A-18937
9	36	75.0	439	3	US-09-004-393B-2
10	36	75.0	446	3	US-09-004-393B-4
11	36	75.0	577	4	US-09-252-991A-20716
12	34	70.8	150	3	US-08-228-986-107
13	34	70.8	150	4	US-10-101-464A-107
14	34	70.8	301	1	US-08-420-235B-47
15	34	70.8	301	2	US-08-343-101A-22
16	34	70.8	301	3	US-09-183-688-22
17	34	70.8	301	3	US-08-793-624-47
18	34	70.8	301	4	US-09-519-489-22
19	34	70.8	506	2	US-08-929-501-2
20	34	70.8	506	3	US-09-140-177-2
21	34	70.8	506	3	US-09-397-979-2
22	34	70.8	590	2	US-08-929-501-12
23	34	70.8	590	3	US-09-140-177-12
24	34	70.8	590	3	US-09-397-979-12
25	34	70.8	1166	4	US-10-101-464A-900
26	33	68.8	61	4	US-09-248-796A-22949
27	33	68.8	94	4	US-09-513-999C-5607

28 33 68.8 128 4 US-09-513-999C-7746 Sequence 7746, Ap  
29 33 68.8 162 3 US-09-366-623-2 Sequence 2, Appli  
30 33 68.8 262 1 US-08-015-973-8 Sequence 8, Appli  
31 33 68.8 262 2 US-08-448-164-8 Sequence 8, Appli  
32 33 68.8 262 3 US-08-081-929-8 Sequence 8, Appli  
33 33 68.8 324 2 US-08-793-410-29 Sequence 29, Appl  
34 33 68.8 324 2 US-08-793-410-30 Sequence 30, Appl  
35 33 68.8 328 2 US-08-793-410-6 Sequence 6, Appli  
36 33 68.8 328 2 US-08-793-410-7 Sequence 7, Appli  
37 33 68.8 330 3 US-09-064-411A-9 Sequence 9, Appli  
38 33 68.8 332 3 US-09-064-411A-13 Sequence 13, Appl  
39 33 68.8 375 1 US-08-464-523B-24 Sequence 24, Appl  
40 33 68.8 383 1 US-08-464-523B-29 Sequence 29, Appl  
41 33 68.8 411 2 US-08-440-845D-3 Sequence 3, Appli  
42 33 68.8 411 2 US-08-440-845D-4 Sequence 4, Appli  
43 33 68.8 411 3 US-08-868-458-3 Sequence 3, Appli  
44 33 68.8 411 3 US-08-868-458-4 Sequence 4, Appli  
45 33 68.8 415 1 US-08-464-523B-27 Sequence 27, Appli

ALIGNMENTS

RESULT 1  
US-09-454-204A-20  
; Sequence 20, Application US/09454204A  
; Patent No. 6663871  
; GENERAL INFORMATION:  
; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg  
; APPLICANT: Plebanski, Magdalena  
; APPLICANT: Hanke, Tomas  
; APPLICANT: Smith, Geoffrey L.  
; APPLICANT: Blanchard, Tom  
; TITLE OF INVENTION: Methods and Reagents for Vaccination  
; FILE REFERENCE: 2907.1000-000  
; CURRENT APPLICATION NUMBER: US/09/454,204A  
; CURRENT FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: PCT/GB98/01681  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: GB 97 11957.2  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 20  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: CTL Epitope of the Malaria String  
US-09-454-204A-20

Query Match 100.0%; Score 48; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 3.8e+05;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9  
|||  
Db 1 HLGNVKYL 9

RESULT 2  
US-09-454-204A-41  
; Sequence 41, Application US/09454204A  
; Patent No. 6663871  
; GENERAL INFORMATION:  
; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg

us-10-042-202-1-rai

Mon Dec 6 15:42:46 2004

APPLICANT: Plebanski, Magdalena  
 APPLICANT: Hanke, Tomas  
 APPLICANT: Smith, Geoffrey L.  
 APPLICANT: Blanchard, Tom  
 TITLE OF INVENTION: Methods and Reagents for Vaccination  
 TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response  
 FILE REFERENCE: 2907.1000-000  
 CURRENT APPLICATION NUMBER: US/09/454.204A  
 CURRENT FILING DATE: 1999-12-09  
 PRIOR APPLICATION NUMBER: PCT/GB98/01681  
 PRIOR FILING DATE: 1998-06-09  
 PRIOR APPLICATION NUMBER: GB 97 11957.2  
 PRIOR FILING DATE: 1997-06-09  
 NUMBER OF SEQ ID NOS: 78  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 41  
 LENGTH: 229  
 TYPE: PRT  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: Complete Epitope of Malaria String  
 US-09-454-204A-41

Query Match 100.0%; Score 48; DB 4; Length 229;  
 Best Local Similarity 100.0%; Pred. No. 0.045;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9  
 DB 88 HLGNVKYL 96

RESULT 3  
 US-08-313-288B-14  
 Sequence 14, Application US/08313288B  
 Patent No. 5750502  
 GENERAL INFORMATION:  
 APPLICANT: Jessell, Thomas M. and Avihu Klar  
 TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A  
 TITLE OF INVENTION: NOVEL SECRETED PROTEIN, P-SPONDIN  
 NUMBER OF SEQUENCES: 20  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Cooper & Dunham LLP  
 STREET: 1185 Avenue of the Americas  
 CITY: New York  
 STATE: New York  
 COUNTRY: USA  
 ZIP: 10036  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/313,288B  
 FILING DATE: January 5, 1995  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: White, John P.  
 REGISTRATION NUMBER: 28,678  
 REFERENCE/DOCKET NUMBER: 40028-A-PCT-US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (212) 278-0400  
 TELEFAX: (212) 391-0526  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 559 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO

ANTI-SENSE: NO  
 US-08-313-288B-14  
 Query Match 100.0%; Score 48; DB 1; Length 559;  
 Best Local Similarity 100.0%; Pred. No. 0.12;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HLGNVKYL 9  
 DB 3 HLGNVKYL 11  
 RESULT 4  
 US-09-009-953-44  
 Sequence 44, Application US/09009953  
 Patent No. 6413517  
 GENERAL INFORMATION:  
 APPLICANT: Sette, Alessandro  
 TITLE OF INVENTION: Identification of Broadly  
 Reactive DR Restricted Epitopes  
 NUMBER OF SEQUENCES: 274  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew LLP  
 STREET: Two Embarcadero Center, Eighth Floor  
 CITY: San Francisco  
 STATE: CA  
 COUNTRY: USA  
 ZIP: 94111-3834  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSeq for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/009,953  
 FILING DATE: 21-Jan-1998  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/036,713  
 FILING DATE: 23-JAN-1997  
 APPLICATION NUMBER: US 60/037,432  
 FILING DATE: 07-FEB-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Weber, Ellen Lauver  
 REGISTRATION NUMBER: 32,762  
 REFERENCE/DOCKET NUMBER: 018623-011520US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-576-0200  
 TELEFAX: 415-576-0300  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 44:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 15 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
 US-09-009-953-44

Query Match 83.3%; Score 40; DB 4; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.092;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGNVKYL 9  
 DB 1 LGNVKYL 8

RESULT 5  
 US-07-846-992-3  
 Sequence 3, Application US/07846992  
 Patent No. 5583046

GENERAL INFORMATION:  
APPLICANT: Valenta, Rudolf  
APPLICANT: Duchene, Michael  
APPLICANT: Pottenburger, Karin  
APPLICANT: Breitenbach, Michael  
APPLICANT: Kraft, Dietrich  
APPLICANT: Rumpold, Helmut  
APPLICANT: Scheiner, Otto  
TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis  
and Therapy of Allergic Diseases  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/846,992  
FILING DATE: 19920606  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/353,844  
FILING DATE: 18-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jones III, Harry C  
REGISTRATION NUMBER: 20,280  
REFERENCE/DOCKET NUMBER: 6530-011  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Betula verrucosa  
FEATURE:  
OTHER INFORMATION: Amino acid sequence identity  
OTHER INFORMATION: with profilin of other organisms is as follows:  
OTHER INFORMATION: 30% with human profilin, 28% with calf and mouse,  
OTHER INFORMATION: 26% with yeast and 25% with Acanthamoeba  
US-07-846-992-3

Query Match 81.2%; Score 39; DB 1; Length 133;  
Best Local Similarity 66.7%; Pred. No. 1.7;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9  
Db 68 HLGKIKYV 76

RESULT 6  
US-08-469-555-3  
Sequence 3, Application US/08469555  
Patent No. 5648242  
GENERAL INFORMATION:  
APPLICANT: Valenta, Rudolf  
APPLICANT: Duchene, Michael  
APPLICANT: Pottenburger, Karin  
APPLICANT: Breitenbach, Michael  
APPLICANT: Kraft, Dietrich

APPLICANT: Rumpold, Helmut  
APPLICANT: Scheiner, Otto  
TITLE OF INVENTION: Birch Pollen Allergen P14 for Diagnosis  
and Therapy of Allergic Diseases  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,555  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/846,992  
FILING DATE: 06-JUN-1992  
APPLICATION NUMBER: US/07/353,844  
FILING DATE: 18-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Jones III, Harry C  
REGISTRATION NUMBER: 20,280  
REFERENCE/DOCKET NUMBER: 6530-011  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864/9741  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Betula verrucosa  
FEATURE:  
OTHER INFORMATION: Amino acid sequence identity  
OTHER INFORMATION: with profilin of other organisms is as follows:  
OTHER INFORMATION: 30% with human profilin, 28% with calf and mouse,  
OTHER INFORMATION: 26% with yeast and 25% with Acanthamoeba  
US-08-469-555-3

Query Match 81.2%; Score 39; DB 1; Length 133;  
Best Local Similarity 66.7%; Pred. No. 1.7;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9  
Db 68 HLGKIKYV 76

RESULT 7  
US-09-328-352-7616  
Sequence 7616, Application US/09328352  
Patent No. 6562958  
GENERAL INFORMATION:  
APPLICANT: Gary L. Breton et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: GTC99-03PA  
CURRENT APPLICATION NUMBER: US/09/328,352  
CURRENT FILING DATE: 1999-06-04  
NUMBER OF SEQ ID NOS: 8252  
SEQ ID NO 7616  
LENGTH: 265

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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7616

Query Match      77.1%; Score 37; DB 4; Length 265;
Best Local Similarity 77.8%; Pred. No. 9.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
   |||:||||
Db 81 HLGVSYL 89

RESULT 8
US-09-248-796A-18937
; Sequence 18937, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18937
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (369)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknd
US-09-248-796A-18937

Query Match      75.0%; Score 36; DB 4; Length 376;
Best Local Similarity 75.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 8
   |||:||||
Db 126 HLGSLKYL 133

RESULT 9
US-09-004-393B-2
; Sequence 2, Application US/09004393B
; Patent No. 6310271
; GENERAL INFORMATION:
; APPLICANT: Hanson D., Andrew
; APPLICANT: Rathinasabapathi, Bala
; APPLICANT: Burnet, Michael
; TITLE OF INVENTION: Polynucleotides Encoding Choline Monoxygenase and
; FILE REFERENCE: UF-162
; CURRENT APPLICATION NUMBER: US/09/004,393B
; CURRENT FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/035,147
; PRIOR FILING DATE: 1997-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-004-393B-2

Query Match      75.0%; Score 36; DB 3; Length 439;
Best Local Similarity 87.5%; Pred. No. 28;
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Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGNVKYL 9
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Db 140 LGNVYL 147

RESULT 10
US-09-004-393B-4
; Sequence 4, Application US/09004393B
; Patent No. 6310271
; GENERAL INFORMATION:
; APPLICANT: Hanson D., Andrew
; APPLICANT: Rathinasabapathi, Bala
; APPLICANT: Burnet, Michael
; TITLE OF INVENTION: Polynucleotides Encoding Choline Monoxygenase and
; FILE REFERENCE: UF-162
; CURRENT APPLICATION NUMBER: US/09/004,393B
; CURRENT FILING DATE: 1998-01-08
; PRIOR APPLICATION NUMBER: 60/035,147
; PRIOR FILING DATE: 1997-01-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-004-393B-4

Query Match      75.0%; Score 36; DB 3; Length 446;
Best Local Similarity 87.5%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGNVKYL 9
   |||:||||
Db 147 LGNVYL 154

RESULT 11
US-09-252-991A-20716
; Sequence 20716, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20716
; LENGTH: 577
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20716

Query Match      75.0%; Score 36; DB 4; Length 577;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGNVKYL 9
   |||:||||
Db 105 LGNIRYL 112

RESULT 12
US-09-228-986-107
; Sequence 107, Application US/09228986
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; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 107
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-107

Query Match          70.8%; Score 34; DB 3; Length 150;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 HLGNVKYL 8
Db      101 HLGNISFL 108

RESULT 13
US-10-101-464A-107
; Sequence 107, Application US/10101464A
; Patent No. 6768041
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-107

Query Match          70.8%; Score 34; DB 4; Length 150;
Best Local Similarity 62.5%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 HLGNVKYL 8
Db      101 HLGNISFL 108

RESULT 14
US-08-420-235B-47
; Sequence 47, Application US/08420235B
; Patent No. 5801042
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: UNIQUE ASSOCIATED KAPOSI'S SARCOMA VIRUS
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
```

```
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/420,235B
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-420-235B-47

Query Match          70.8%; Score 34; DB 1; Length 301;
Best Local Similarity 75.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 HLGNVKYL 8
Db      175 HLGSVSYL 182

RESULT 15
US-08-343-101A-22
; Sequence 22, Application US/08343101A
; Patent No. 5830759
; GENERAL INFORMATION:
; APPLICANT: Chang, Yuan
; APPLICANT: Moore, Patrick S.
; TITLE OF INVENTION: Unique Associated Kaposi's Sarcoma
; TITLE OF INVENTION: Virus Sequences And Uses Thereof
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/343,101A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq., John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45185-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-278-0400
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us-10-042-202-1.rai

Mon Dec 6 15:42:46 2004

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; TELEFAX: 212-391-0526
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 301 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-343-101A-22

Query Match      70.8%   Score 34; DB 2; Length 301;
Best Local Similarity 75.0%   Pred. No. 46;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 HLGNVKYL 8
      |||:|
Db      175 HLGSVSYL 182

Search completed: December 6, 2004, 15:32:09
Job time : 28.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:26:21 ; Search time 99 Seconds  
(without alignments)  
32.420 Million cell updates/sec

Title: US-10-042-202-1  
Perfect score: 48  
Sequence: 1 HLGNVKYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	48	100.0	9	13	US-10-042-202-1
2	48	100.0	9	14	US-10-079-167-20
3	48	100.0	9	16	US-10-653-624-20
4	48	100.0	9	16	US-10-777-053-508
5	48	100.0	9	16	US-10-833-439-20
6	48	100.0	9	17	US-10-833-745-20
7	48	100.0	9	17	US-10-833-744-20
8	48	100.0	9	17	US-10-837-217-508
9	48	100.0	9	17	US-10-686-943-20
10	48	100.0	15	14	US-10-360-835-6
11	48	100.0	20	14	US-10-079-167-89
12	48	100.0	20	15	US-10-345-000-11
13	48	100.0	229	14	US-10-079-167-41
					Sequence 1, Appl
					Sequence 20, Appl
					Sequence 20, Appl
					Sequence 508, App
					Sequence 20, Appl
					Sequence 20, Appl
					Sequence 20, Appl
					Sequence 508, App
					Sequence 20, Appl
					Sequence 6, Appl
					Sequence 89, Appl
					Sequence 11, Appl
					Sequence 41, Appl

14	48	100.0	229	16	US-10-653-624-41	Sequence 41, Appl
15	48	100.0	229	16	US-10-833-439-41	Sequence 41, Appl
16	48	100.0	229	17	US-10-833-745-41	Sequence 41, Appl
17	48	100.0	229	17	US-10-833-744-41	Sequence 41, Appl
18	48	100.0	229	17	US-10-686-943-41	Sequence 41, Appl
19	42	87.5	1474	16	US-10-437-963-164906	Sequence 164906,
20	40	83.3	15	13	US-10-103-395-44	Sequence 44, Appl
21	39	81.2	133	10	US-09-847-208-44	Sequence 44, Appl
22	38	79.2	1006	15	US-10-287-226-318	Sequence 318, App
23	37	77.1	312	14	US-10-024-212-150	Sequence 150, App
24	37	77.1	326	14	US-10-306-762-191	Sequence 191, App
25	36	75.0	317	14	US-10-369-493-6984	Sequence 6984, Ap
26	36	75.0	432	15	US-10-389-566-1588	Sequence 1588, Ap
27	36	75.0	475	15	US-10-602-268-19	Sequence 20, Appl
28	36	75.0	484	15	US-10-602-268-20	Sequence 20, Appl
29	36	75.0	536	9	US-09-815-242-11929	Sequence 11929, A
30	36	75.0	536	15	US-10-282-122A-66501	Sequence 66501, A
31	36	75.0	2416	14	US-10-032-585-7352	Sequence 7352, Ap
32	35	72.9	256	17	US-10-425-115-191246	Sequence 191246,
33	35	72.9	555	15	US-10-282-122A-68210	Sequence 68210, A
34	35	72.9	619	16	US-10-767-701-46541	Sequence 46541, A
35	35	72.9	623	17	US-10-425-115-233059	Sequence 233059,
36	35	72.9	643	15	US-10-425-114-63190	Sequence 63190, A
37	35	72.9	645	15	US-10-425-114-55223	Sequence 55223, A
38	35	72.9	645	15	US-10-425-114-58005	Sequence 58005, A
39	35	72.9	645	15	US-10-425-114-59639	Sequence 59639, A
40	35	72.9	670	15	US-10-080-334-165	Sequence 165, App
41	35	72.9	734	14	US-10-028-248A-108	Sequence 108, App
42	35	72.9	734	15	US-10-107-782-108	Sequence 108, App
43	35	72.9	765	13	US-10-044-303-1	Sequence 1, Appl
44	35	72.9	1016	13	US-10-044-303-2	Sequence 2, Appl
45	35	72.9	1017	14	US-10-369-493-5684	Sequence 5684, Ap

ALIGNMENTS

RESULT 1

US-10-042-202-1  
; Sequence 1, Application US/10042202  
; Publication No. US20020136733A1  
; GENERAL INFORMATION:  
; APPLICANT: Adrian Vivian Sinton Hill, Michael AIDOO,  
; Catherine Elizabeth Margaret Allisopp, Ajit LALVANI, Magdalena  
; PLEBANSKI, Hilton Carter WHITTLE,  
; TITLE OF INVENTION: MALARIA PEPTIDES  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.  
; STREET: 2033 K Street,N.W., Suite 800,  
; CITY: Washington  
; STATE: D.C.,  
; COUNTRY: U.S.A.  
; ZIP: 20006-1021  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WordPad for Windows 95  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/042,202  
; FILING DATE: 11-Jan-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/714,175  
; FILING DATE: 28-JAN-1997  
; APPLICATION NUMBER: WO PCT/GB95/26982  
; FILING DATE: 30-MAR-1995  
; APPLICATION NUMBER: GB 9406492.0  
; FILING DATE: 31-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Warren M Cheek, Jr.  
; REGISTRATION NUMBER: 33,367  
; REFERENCE/DOCKET NUMBER: 2002\_0026

us-10-042-202-1.1.rapb

Mon Dec 6 15:42:47 2004

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)-721-8200
; TELEFAX: (202)-721-8250
; TELEX: <unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-042-202-1
Query Match 100.0%; Score 48; DB 13; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9
Db 1 HLGNVKYL 9

RESULT 2
US-10-079-167-20
; Sequence 20, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-08-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-079-167-20
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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9
Db 1 HLGNVKYL 9

RESULT 3
US-10-653-624-20
; Sequence 20, Application US/10653624
; Publication No. US20040131594A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.

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```

; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Jorg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/653,624
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/454,204A
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-653-624-20
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Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9
Db 1 HLGNVKYL 9

RESULT 4
US-10-777-053-508
; Sequence 508, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; TITLE OF INVENTION: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; FILE REFERENCE: MANK 022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; CURRENT FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 508
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Plasmodium Faciparum
US-10-777-053-508
Query Match 100.0%; Score 48; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9
Db 1 HLGNVKYL 9

RESULT 5
US-10-833-439-20

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; Sequence 20, Application US/10833439
; Publication No. US20040175365A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Jorg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/833,439
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/10/686,943
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-439-20

Query Match 100.0%; Score 48; DB 16; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL V 9
Db 1 HLGNVKYL V 9

RESULT 7
US-10-833-744-20
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; Publication No. US20040197349A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Jorg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/833,744
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/10/686,943
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-744-20

Query Match 100.0%; Score 48; DB 17; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL V 9
Db 1 HLGNVKYL V 9

RESULT 8
US-10-837-217-508
; Sequence 508, Application US/10837217
; Publication No. US20040203051A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANNK.022C2
; CURRENT APPLICATION NUMBER: US/10/837,217
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US-10-042-202-1.rapb

Mon Dec 6 15:42:47 2004

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; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
; TITLE OF INVENTION: AND MALINGNANCIES
; FILE REFERENCE: 5986/1J876
; CURRENT APPLICATION NUMBER: US/10/360,836
; PRIOR FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/354,963
; PRIOR FILING DATE: 2002-02-08
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Plasmodium
; US-10-360-836-6

Query Match      100.0%; Score 48; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
Db 3 HLGNVKYL 11

RESULT 11
US-10-079-167-89
; Sequence 89, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Peptide No. US20030138454A1 1 in the TTI-10 pool
; US-10-079-167-89

Query Match      100.0%; Score 48; DB 14; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
Db 3 HLGNVKYL 11

RESULT 12
US-10-345-000-11
; Sequence 11, Application US/10345000
; Publication No. US20040018177A1
; GENERAL INFORMATION:
; APPLICANT: OXON PHARMACEUTICALS LIMITED
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE

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; TITLE OF INVENTION: VACCINATION METHOD
; FILE REFERENCE: 550-409
; CURRENT APPLICATION NUMBER: US/10/345,000
; CURRENT FILING DATE: 2003-02-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-10-345-000-11
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Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HLGNVKYL 9
Db 3 HLGNVKYL 11
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RESULT 13
US-10-079-167-41
; Sequence 41, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen C.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
US-10-079-167-41
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Query Match 100.0%; Score 48; DB 14; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HLGNVKYL 9
Db 88 HLGNVKYL 96
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RESULT 14
US-10-653-624-41
; Sequence 41, Application US/10653624
; Publication No. US20040131594A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Joerg
```

```
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/653,624
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/454,204A
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
US-10-653-624-41
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Query Match 100.0%; Score 48; DB 16; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 HLGNVKYL 9
Db 88 HLGNVKYL 96
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RESULT 15
US-10-833-439-41
; Sequence 41, Application US/10833439
; Publication No. US20040175365A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Joerg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/833,439
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/10/686,943
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
US-10-833-439-41
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Query Match 100.0%; Score 48; DB 16; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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us-10-042-202-1.rapb

Mon Dec 6 15:42:47 2004

Qy 1 HLGKVKYLV 9  
| | | | |  
Db 88 HLGKVKYLV 96

Search completed: December 6, 2004, 15:36:07  
Job time : 100 secs



GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:18:43 ; Search time 23.5 seconds  
(without alignments)  
36.849 Million cell updates/sec

Title: US-10-042-202-1  
Perfect score: 48  
Sequence: 1 HLGNVKYL V 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	559	2 S04531	thrombospondin-rel
2	48	100.0	574	2 A46283	sporozoite surface
3	39	81.2	133	2 JC2082	profilin - Europea
4	39	81.2	427	2 C45438	myosin I gamma, MM
5	39	81.2	1006	2 A53933	myosin I myr 4 - r
6	37	77.1	384	2 S63345	hypothetical prote
7	37	77.1	450	2 T25693	hypothetical prote
8	36	75.0	131	2 T10769	profilin - Para ru
9	36	75.0	317	2 T22736	hypothetical prote
10	36	75.0	439	2 T09214	choline monooxygen
11	36	75.0	446	2 T14542	choline monooxygen
12	36	75.0	495	2 T27936	hypothetical prote
13	36	75.0	536	2 D83196	conserved hypothet
14	36	75.0	2139	2 T18296	myosin heavy chain
15	35	72.9	347	2 D39999	hypothetical prote
16	35	72.9	408	2 T21412	hypothetical prote
17	35	72.9	1017	2 T24349	myosin IA - Caenor
18	35	72.9	2116	2 A26655	myosin heavy chain
19	34	70.8	301	2 S33042	hypothetical prote
20	34	70.8	348	2 T15219	hypothetical prote
21	34	70.8	461	2 H81319	probable ADP-hepto
22	34	70.8	560	2 E97776	hypothetical prote
23	34	70.8	560	2 H71702	hypothetical prote
24	34	70.8	604	2 A13653	ATP-dependent RNA
25	34	70.8	785	2 A29953	alpha-i proteinase
26	34	70.8	2626	2 T31099	myosin-RhoGAP prot
27	33	68.8	123	2 S29714	guanine-nucleotide
28	33	68.8	162	2 B95230	phosphopantetheine
29	33	68.8	188	2 S51821	myosin heavy chain

30	33	68.8	222	2 A83906	hypothetical prote
31	33	68.8	285	2 D64557	dipeptide ABC tran
32	33	68.8	308	1 CRHU6	carbonate dehydrat
33	33	68.8	311	2 T24947	hypothetical prote
34	33	68.8	402	2 AH0896	propionate kinase
35	33	68.8	412	2 A59034	oleoyl-lacyl-carri
36	33	68.8	430	2 T12583	oleoyl-lacyl-carri
37	33	68.8	494	2 B96534	hypothetical prote
38	33	68.8	544	2 B84825	probable ABC trans
39	33	68.8	566	2 A81682	conserved hypothet
40	33	68.8	566	2 AS9285	myosin-VIIa motor
41	33	68.8	617	2 S62003	probable ATP-depen
42	33	68.8	733	2 C89940	hypothetical prote
43	33	68.8	843	2 T32487	hypothetical prote
44	33	68.8	1203	2 A59257	myosin VIIa, short
45	33	68.8	1490	2 E84726	probable unconvet

ALIGNMENTS

RESULT 1

S04531  
thrombospondin-related protein TRAP - malaria parasite (Plasmodium falciparum)  
N:Alternate names: thrombospondin-related anonymous protein  
C:Species: Plasmodium falciparum  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S04531

R:Robson, K.J.H.; Hall, J.R.S.; Jennings, M.W.; Harris, T.J.R.; Marsh, K.; Newbold, C.I.,  
Nature 335, 79-82, 1988  
A:Title: A highly conserved amino-acid sequence in thrombospondin, properdin and in prote  
A:Reference number: S04531; MUID:88318952; PMID:3045563  
A:Accession: S04531  
A:Molecule type: DNA  
A:Residues: 1-559 <ROB>  
A:Cross-references: UNIPROT:P16893; EMBL:X13022; NID:g9977; PID:g9978  
F:240-287/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 100.0%; Score 48; DB 2; Length 559;  
Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 HLGNVKYL V 9  
|||  
DB 3 HLGNVKYL V 11

RESULT 2

A46283  
sporozoite surface protein 2 - malaria parasite (Plasmodium falciparum) (strain NFS4)  
N:Alternate names: thrombospondin-related anonymous protein (TRAP)  
C:Species: Plasmodium falciparum  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: A46283  
R:Rogers, W.O.; Malik, A.; Mellouk, S.; Nakamura, K.; Rogers, M.D.; Szarfman, A.; Gordon,  
Proc. Natl. Acad. Sci. U.S.A. 89, 9176-9180, 1992  
A:Title: Characterization of Plasmodium falciparum sporozoite surface protein 2.  
A:Reference number: A46283; MUID:93028427; PMID:1409621

A:Accession: A46283  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-574 <ROG>  
A:Cross-references: UNIPROT:Q26020; GB:M94013; NID:gi160690; PID:gi160691  
F:240-287/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 100.0%; Score 48; DB 2; Length 574;  
Best Local Similarity 100.0%; Pred. No. 0.15; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0;

QY 1 HLGNVKYL V 9  
|||  
DB 3 HLGNVKYL V 11

RESULT 3  
JC2082  
profilin - European white birch  
N/Alternate names: actin-binding protein  
C/Species: Betula pendula (European white birch)  
C/Date: 14-Jul-1994 #sequence\_revision 14-Jul-1994 #text\_change 09-Jul-2004  
C/Accession: JC2082  
R/Valenta, R.; Ball, T.; Vrtala, S.; Duchene, M.; Kraft, D.; Scheiner, O.  
Biochem. Biophys. Res. Commun. 199, 106-118, 1994  
A/Title: cDNA cloning and expression of timothy grass (Phleum pratense) pollen profilin  
A/Reference number: JC2080; MUID:94168560; PMID:8123000  
A/Accession: JC2082  
A/Molecule type: mRNA  
A/Residues: 1-133 <VAL>  
A/Cross-references: UNIPROT:P25816  
A/Experimental source: pollen  
C/Comment: This protein is responsible for cross-reactivities in 20% of pollen and food  
C/Superfamily: profilin  
C/Keywords: actin binding; cytoskeleton

Query Match 81.2%; Score 39; DB 2; Length 133;  
Best Local Similarity 66.7%; Pred. No. 2;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLGNNKYLIV 9  
|||:|:|:  
Db 68 HLGGIKYMV 76

RESULT 4  
C45438  
myosin I gamma, MMI gamma - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 22-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Mar-2004  
C/Accession: C45438  
R/Sheer, E.H.; Joyce, M.P.; Greene, L.A.  
J. Cell Biol. 120, 1405-1416, 1993  
A/Title: Mammalian myosin I alpha, I beta, and I gamma: new widely expressed genes of the  
A/Reference number: A45438; MUID:93194946; PMID:8449986  
A/Accession: C45438  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: nucleic acid  
A/Residues: 1-427 <SHE>  
A/Note: sequence extracted from NCBI backbone (NCBIP:131912)  
F/1-427/Domain: myosin motor domain homology (fragment) <MMOT>

Query Match 81.2%; Score 39; DB 2; Length 427;  
Best Local Similarity 66.7%; Pred. No. 6.8;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNNKYLIV 9  
|||:|:|:  
Db 132 HLGNNKYLIV 140

RESULT 5  
A53933  
myosin I myr 4 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 02-Feb-2001  
C/Accession: A53933  
R/Bachler, M.; Kroschewski, R.; Stoeffler, H.E.; Behrmann, T.  
J. Cell Biol. 126, 375-389, 1994  
A/Title: Rat myr 4 defines a novel subclass of myosin I: identification, distribution, and  
A/Reference number: A53933; MUID:94308268; PMID:8034741  
A/Accession: A53933  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-1006 <BAE>  
A/Cross-references: GB:X71997; NID:G516395; PID:G516396  
C/Superfamily: brush border myosin heavy chain I; myosin motor domain homology  
C/Keywords: nucleotide binding; P-loop

F/12-682/Domain: myosin motor domain homology <MMOT>  
F/102-109/Region: nucleotide-binding motif A (P-loop)

Query Match 81.2%; Score 39; DB 2; Length 1006;  
Best Local Similarity 66.7%; Pred. No. 17;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNNKYLIV 9  
|||:|:|:  
Db 276 HLGNNKYLIV 284

RESULT 6  
S63345  
hypothetical protein YNR015w - yeast (Saccharomyces cerevisiae)  
N/Alternate names: hypothetical protein N2065  
C/Species: Saccharomyces cerevisiae  
C/Date: 27-Apr-1996 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004  
C/Accession: S63345; S63343; S63346  
R/Duesterhoeft, A.; Floeth, M.; Fritze, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.  
submitted to the Protein Sequence Database, April 1996  
A/Reference number: S62944  
A/Accession: S63345  
A/Molecule type: DNA  
A/Residues: 1-354 <DUE>  
A/Cross-references: UNIPROT:P53720; EMBL:Z71630; MIPS:YNR015w  
A/Experimental source: strain S288C  
R/Maurer, C.T.C.; Urbanus, J.H.M.; Planta, R.J.  
submitted to the Protein Sequence Database, April 1996  
A/Reference number: S63266  
A/Accession: S63343  
A/Molecule type: DNA  
A/Residues: 1-58 <MAU>  
A/Cross-references: EMBL:Z71630; MIPS:YNR015w  
A/Experimental source: strain S288C  
R/Pohl, T.M.  
submitted to the Protein Sequence Database, April 1996  
A/Reference number: S63346  
A/Accession: S63346  
A/Molecule type: DNA  
A/Residues: 336-384 <POH>  
A/Cross-references: EMBL:Z71630; MIPS:YNR015w  
A/Experimental source: strain S288C  
C/Genetics:  
A/Gene: SGD:SMW1  
A/Cross-references: SGD:S0005298; MIPS:YNR015w  
A/Map position: 14R

Query Match 77.1%; Score 37; DB 2; Length 384;  
Best Local Similarity 55.6%; Pred. No. 15;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLGNNKYLIV 9  
|||:|:|:  
Db 289 HLGNNKYLIV 297

RESULT 7  
T25693  
hypothetical protein F15A8.7 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T25693  
R/Miller, N.  
submitted to the EMBL Data Library, April 1997  
A/Description: The sequence of C. elegans cosmid F15A8.  
A/Reference number: Z20069  
A/Accession: T25693  
A/Status: preliminary; translated from GB/EMBL/DDBJ  
A/Molecule type: DNA  
A/Residues: 1-450 <ML>  
A/Cross-references: UNIPROT:O02150; EMBL:U97549; PIDN:AAB52849.1; GSPDB:GNO0028; CESP:F15A8  
A/Experimental source: strain Bristol N2; clone F15A8

C;Genetics:  
A;Gene: CESP:F15A8.7  
A;Map position: X  
A;Introns: 30/3; 80/3; 140/2; 172/1; 250/3; 285/3; 375/3  
Query Match 77.1%; Score 37; DB 2; Length 450;  
Best Local Similarity 66.7%; Pred. No. 18;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HLGKVKYLV 9  
|:|:|:|:|  
Db 240 HIGDVEYLV 248  
RESULT 8  
T10769  
profilin - Para rubber tree  
C;Species: Hevea brasiliensis (Para rubber tree)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C;Accession: T10769  
R;Asturias, J.A.; Arilla, M.C.; Gomez-Bayon, N.; Martinez, J.; Martinez, A.; Palacios, R.  
submitted to the EMBL Data Library, October 1997  
A;Description: Cloning and expression of profilin allergen from Hevea brasiliensis.  
A;Reference number: Z17130  
A;Accession: T10769  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-131 <AST>  
A;Cross-references: UNIPROT:O65812; EMBL:Y15042  
A;Experimental source: cv. RRIC 133; pollen  
C;Superfamily: profilin  
C;Keywords: actin binding; cytoskeleton  
Query Match 75.0%; Score 36; DB 2; Length 131;  
Best Local Similarity 66.7%; Pred. No. 7.9;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HLGKVKYLV 9  
|:|:|:|:|  
Db 66 HLGCTKYMV 74  
RESULT 9  
T22736  
hypothetical protein F55F3.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22736  
R;Steward, C.  
submitted to the EMBL Data Library, November 1996  
A;Reference number: Z19607  
A;Accession: T22736  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-317 <WIL>  
A;Cross-references: UNIPROT:Q9XUY5; EMBL:Z81550; PIDN: CAB04477.1; GSPDB:GN00028; CESP:FE  
A;Experimental source: clone F55F3  
C;Genetics:  
A;Gene: CESP:F55F3.3  
A;Map position: X  
A;Introns: 13/3; 47/1; 94/1; 185/3; 228/3; 264/3  
C;Superfamily: Na+/K+-transporting ATPase beta chain  
Query Match 75.0%; Score 36; DB 2; Length 317;  
Best Local Similarity 75.0%; Pred. No. 20;  
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 HLGKVKYL 8  
|:|:|:|:|  
Db 235 HLGKVKYII 242  
RESULT 10

T09214  
choline monooxygenase (EC 1.1.1.3 -) precursor - spinach  
C;Species: Spinacia oleracea (spinach)  
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004  
C;Accession: T09214  
R;Rathinasabapathi, B.; Burnet, M.; Russell, B.L.; Gage, D.A.; Liao, P.C.; Nye, G.J.; Scott, P.C.  
Proc. Natl. Acad. Sci. U.S.A. 94, 3454-3458, 1997  
A;Title: Choline monooxygenase, an unusual iron-sulfur enzyme catalyzing the first step  
A;Reference number: Z16612; MUID:97250559; PMID:9096415  
A;Accession: T09214  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-439 <RAT>  
A;Cross-references: UNIPROT:O04121; EMBL:U85780; NID:G1943944; PIDN:AAB52509.1; PID:G194  
A;Note: parts of this sequence, including the amino end of the mature protein, were deter  
C;Keywords: 2Fe-2S; chloroplast; metalloprotein; oxidoreductase; Rieske iron-sulfur prote  
F;1-60/Domain: transit peptide (chloroplast) #status predicted <TRP>  
F;61-439/Product: choline monooxygenase #status experimental <MAT>  
F;152-199/Domain: Rieske [2Fe-2S] homology <RSK>  
F;162,164,181,184/Binding site: 2Fe-2S cluster (Cys, His, Cys, His) (covalent) #status p  
Query Match 75.0%; Score 36; DB 2; Length 439;  
Best Local Similarity 87.5%; Pred. No. 28;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LGNVKYL 9  
|:|:|:|:|  
Db 140 LGNVKYL 147  
RESULT 11  
T14542  
choline monooxygenase - beet  
C;Species: Beta vulgaris (beet)  
C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: T14542  
R;Russell, B.L.; Rathinasabapathi, B.; Hanson, A.D.  
submitted to the EMBL Data Library, September 1997  
A;Description: Osmotic stress induces expression of choline monooxygenase in sugar beet  
A;Reference number: Z18128  
A;Accession: T14542  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-446 <RUS>  
A;Cross-references: UNIPROT:O22553; EMBL:AF023132; NID:G2522209; PID:G2522210  
A;Experimental source: strain Great Western D-2; salinized leaves  
A;Note: expression induced by osmotic stress  
C;Keywords: monooxygenase  
Query Match 75.0%; Score 36; DB 2; Length 446;  
Best Local Similarity 87.5%; Pred. No. 28;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 LGNVKYL 9  
|:|:|:|:|  
Db 147 LGNVKYL 154  
RESULT 12  
T27936  
hypothetical protein ZK622.3 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T27936  
R;Leimbach, D.  
submitted to the EMBL Data Library, November 1995  
A;Description: The sequence of C. elegans cosmid ZK622.  
A;Reference number: Z20443  
A;Accession: T27936  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-495 <LEI>

A;Cross-references: UNIPROT:Q23552; EMBL:U39998; PIDN:AAA81102.1; CESP:ZK622.3

C;Genetics:

A;Gene: CESP:ZK622.3

A;Introns: 34/2; 97/2; 222/3; 310/3

C;Superfamily: Caenorhabditis elegans hypothetical protein ZK622.3

Query Match 75.0%; Score 36; DB 2; Length 495;

Best Local Similarity 66.7%; Pred. No. 32; Gaps 0;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9

||||:|

Db 129 HLGNIYQV 137

RESULT 13

D83196

conserved hypothetical protein PA3602 [imported] - Pseudomonas aeruginosa (strain PAO1)

C;Species: Pseudomonas aeruginosa

C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 16-Aug-2004

C;Accession: D83196

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic patho

A;Reference number: A82950; MUID:2043737; PMID:10984043

A;Accession: D83196

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-536 <STO>

A;Cross-references: UNIPROT:Q9HY24; GB:AE004780; GB:AE004091; NID:g9949749; PIDN:AA0699

A;Experimental source: strain PAO1

C;Genetics:

A;Gene: PA3602

C;Superfamily: Glutamate synthase, large subunit domain 2

Query Match

Best Local Similarity 75.0%; Score 36; DB 2; Length 536;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGNVKYL 9

||||:|

Db 64 LGNIYLV 71

RESULT 14

T18296

myosin heavy chain - Entamoeba histolytica

C;Species: Entamoeba histolytica

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T18296

R;Guillen, N.

submitted to the EMBL Data Library, February 1997

A;Reference number: Z18865

A;Accession: T18296

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2139 <GUI>

A;Cross-references: UNIPROT:Q07569; EMBL:L03534; NID:g1850912; PID:g1850913; PIDN:AAB480

C;Genetics:

A;Gene: mbca

C;Superfamily: myosin heavy chain; myosin motor domain homology

F;91-780/Domain: myosin motor domain homology <WMO>

Query Match

Best Local Similarity 85.7%; Score 36; DB 2; Length 2139;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKY 7

||||:|

Db 363 HLGNIYLV 369

RESULT 15

D39999

hypothetical protein 4 - Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii, Chlamydia psittaci

C;Date: 08-Nov-1991 #sequence\_revision 08-Nov-1991 #text\_change 09-Jul-2004

C;Accession: S18145; D39999

R;Lusher, M.R.; Gregory, J.; Storey, C.C.; Richmond, S.J.

submitted to the EMBL Data Library, October 1991

A;Description: Analysis of the complete nucleotide sequence of the plasmid pCpA1 isolate

A;Reference number: S18141

A;Accession: S18145

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-347 <LUS>

A;Cross-references: UNIPROT:Q46260; EMBL:X62475; NID:g40608; PIDN:CAA44336.1; PID:g40613

Query Match

Best Local Similarity 72.9%; Score 35; DB 2; Length 347;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9

||||:|

Db 134 HLGNIYLV 142

Search completed: December 6, 2004, 15:31:09

Job time : 25.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

# OM protein - protein search, using sw model

Run on: December 6, 2004, 15:17:52 ; Search time 125.5 Seconds  
(without alignments)  
41.262 Million cell updates/sec

Title: US-10-042-202-1  
Perfect score: 48  
Sequence: 1 HLGNVKYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_02: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	323	2 Q70GK0	Q70GK0 plasmodium
2	48	100.0	323	2 CAE46495	CAE46495 plasmodium
3	48	100.0	327	2 Q70GJ7	Q70GJ7 plasmodium
4	48	100.0	327	2 CAE46498	CAE46498 plasmodium
5	48	100.0	331	2 Q70GE3	Q70GE3 plasmodium
6	48	100.0	331	2 Q70GJ8	Q70GJ8 plasmodium
7	48	100.0	331	2 Q70GJ9	Q70GJ9 plasmodium
8	48	100.0	331	2 Q70GK1	Q70GK1 plasmodium
9	48	100.0	331	2 Q70GK2	Q70GK2 plasmodium
10	48	100.0	331	2 Q70GK3	Q70GK3 plasmodium
11	48	100.0	331	2 CAE46492	CAE46492 plasmodium
12	48	100.0	331	2 CAE46493	CAE46493 plasmodium
13	48	100.0	331	2 CAE46494	CAE46494 plasmodium
14	48	100.0	331	2 CAE46496	CAE46496 plasmodium
15	48	100.0	331	2 CAE46497	CAE46497 plasmodium
16	48	100.0	331	2 CAE46626	CAE46626 plasmodium
17	48	100.0	559	1 TRAP_PLAFA	P16893 plasmodium
18	48	100.0	559	2 Q76109	Q76109 plasmodium
19	48	100.0	559	2 Q76111	Q76111 plasmodium
20	48	100.0	559	2 Q76112	Q76112 plasmodium
21	48	100.0	559	2 Q76113	Q76113 plasmodium
22	48	100.0	559	2 Q76114	Q76114 plasmodium
23	48	100.0	559	2 Q76117	Q76117 plasmodium
24	48	100.0	559	2 Q76118	Q76118 plasmodium
25	48	100.0	559	2 Q01502	Q01502 plasmodium
26	48	100.0	559	2 Q01503	Q01503 plasmodium
27	48	100.0	559	2 Q01506	Q01506 plasmodium
28	48	100.0	559	2 Q01508	Q01508 plasmodium
29	48	100.0	559	2 Q01509	Q01509 plasmodium
30	48	100.0	559	2 Q717T6	Q717T6 plasmodium
31	48	100.0	559	2 Q717T7	Q717T7 plasmodium

32 48 100.0 559 2 Q717T9  
33 48 100.0 559 2 Q717U0  
34 48 100.0 559 2 Q9TYC1  
35 48 100.0 559 2 Q9TYC2  
36 48 100.0 559 2 Q9TYC3  
37 48 100.0 559 2 Q9TYC4  
38 48 100.0 559 2 Q9TYC5  
39 48 100.0 559 2 Q9TYC6  
40 48 100.0 559 2 Q9TYC7  
41 48 100.0 559 2 Q9TYC8  
42 48 100.0 559 2 Q9TYD0  
43 48 100.0 559 2 Q9TYD1  
44 48 100.0 559 2 Q9TYD2  
45 48 100.0 559 2 Q9GTW7

Q717T9 plasmodium  
Q717U0 plasmodium  
Q9TYC1 plasmodium  
Q9TYC2 plasmodium  
Q9TYC3 plasmodium  
Q9TYC4 plasmodium  
Q9TYC5 plasmodium  
Q9TYC6 plasmodium  
Q9TYC7 plasmodium  
Q9TYC8 plasmodium  
Q9TYD0 plasmodium  
Q9TYD1 plasmodium  
Q9TYD2 plasmodium  
Q9GTW7 plasmodium

## ALIGNMENTS

RESULT 1  
Q70GK0 PRELIMINARY; PRT; 323 AA.  
AC Q70GK0;  
DT 05-JUL-2004 (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Trap protein (Fragment).  
GN Name=trap;  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mamillapalli A., Joshi H., Malhotra P.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ581768; CAE46495.1;  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR002035; VWF A.  
DR Pfam; PF00090; TSP\_1; 1.  
DR Pfam; PF00092; VWA\_1; 1.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR SMART; SM00209; TSP1; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50092; TSP1; 1.  
DR PROSITE; PS50234; VWEA; 1.  
FT NON\_TER 323 323  
SQ SEQUENCE 323 AA; 36608 MW; 02A0030CCE5EDCA93 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 323;  
Best Local Similarity 100.0%; Pred. No. 0.43;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9  
Db 3 HLGNVKYL 11

RESULT 2  
CAE46495 PRELIMINARY; PRT; 323 AA.  
ID CAE46495  
AC CAE46495;  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE Trap protein (Fragment).  
GN TRAP.  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BM3-62;  
RA Mamillapalli A., Joshi H., Malhotra P.;

```
RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in
RT Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581771; CAE46498.1; -.
FT NON_TER 323 327
SQ SEQUENCE 323 AA; 36608 MW; 02A0030CC5EDCA93 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 323;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
Db 3 HLGNVKYL 11

RESULT 3
Q70GJ7 PRELIMINARY; PRT; 327 AA.
AC Q70GJ7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Trap protein (Fragment).
GN Name=trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581771; CAE46498.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP 1; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSP1; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER 327 327
SQ SEQUENCE 327 AA; 37251 MW; 881D7A4B4EDD235A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
Db 3 HLGNVKYL 11

RESULT 4
CAE46498 PRELIMINARY; PRT; 327 AA.
AC CAE46498;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DT 02-MAR-2004 (TREMBlrel. 27, Last annotation update)
DE Trap protein (Fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DK3-16;
RA Mamillapalli A., Joshi H., Malhotra P.;
RT "Polymorphism in TRAP N-terminal region of Plasmodium falciparum in
RT Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in
RT Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581771; CAE46498.1; -.
FT NON_TER 323 327
SQ SEQUENCE 323 AA; 37251 MW; 881D7A4B4EDD235A CRC64;

Query Match 100.0%; Score 48; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
Db 3 HLGNVKYL 11

RESULT 5
Q70GE3 PRELIMINARY; PRT; 331 AA.
AC Q70GE3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Trombospondin-related protein (Fragment).
GN Name=trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ582081; CAE46626.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP 1; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER 331 331
SQ SEQUENCE 331 AA; 37559 MW; B1BFCC93B8BD4D25 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
Db 3 HLGNVKYL 11

RESULT 6
Q70GJ8 PRELIMINARY; PRT; 331 AA.
AC Q70GJ8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Trap protein (Fragment).
GN Name=trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581770; CAE46497.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP 1; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
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DR SMART; SM00209; TSP1; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50092; TSP1; 1.  
DR PROSITE; PS50234; VWA; 1.  
FT NON-TER 331  
SQ SEQUENCE 331 AA; 37521 MW; CBD1823A0C8C49EB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 HLGNVKYL 9  
Db 3 HLGNVKYL 11

## RESULT 7

Q70GJ9  
ID Q70GJ9 PRELIMINARY; PRT; 331 AA.  
AC Q70GJ9;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Trap protein (Fragment).  
GN Name-trap;  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mamillapalli A., Joshi H., Malhotra P.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ581769; CAE46496.1; --  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00090; TSP1; 1.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR SMART; SM00209; TSP1; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50092; TSP1; 1.  
DR PROSITE; PS50234; VWA; 1.  
FT NON-TER 331  
SQ SEQUENCE 331 AA; 37573 MW; 60EBBAC3FDD9C779 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 HLGNVKYL 9  
Db 3 HLGNVKYL 11

## RESULT 8

Q70GK1  
ID Q70GK1 PRELIMINARY; PRT; 331 AA.  
AC Q70GK1;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Trap protein (Fragment).  
GN Name-trap;  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mamillapalli A., Joshi H., Malhotra P.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ581767; CAE46494.1; --  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR002035; VWF\_A.

DR Pfam; PF00090; TSP1; 1.  
DR Pfam; PF00092; VWA; 1.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR SMART; SM00209; TSP1; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50092; TSP1; 1.  
DR PROSITE; PS50234; VWA; 1.  
FT NON-TER 331  
SQ SEQUENCE 331 AA; 37601 MW; 39EBBACF0DD9C77C CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 HLGNVKYL 9  
Db 3 HLGNVKYL 11

## RESULT 9

Q70GK2  
ID Q70GK2 PRELIMINARY; PRT; 331 AA.  
AC Q70GK2;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Trap protein (Fragment).  
GN Name-trap;  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mamillapalli A., Joshi H., Malhotra P.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ581765; CAE46493.1; --  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR002035; VWF\_A.  
DR Pfam; PF00090; TSP1; 1.  
DR Pfam; PF00092; VWA; 1.  
DR PRINTS; PR00453; VWFADOMAIN.  
DR SMART; SM00209; TSP1; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS50092; TSP1; 1.  
DR PROSITE; PS50234; VWA; 1.  
FT NON-TER 331  
SQ SEQUENCE 331 AA; 37609 MW; 2FE4EB47F1963D76 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;  
Best Local Similarity 100.0%; Pred. No. 0.44; Mismatches 0; Indels 0; Gaps 0;  
Matches 9; Conservative 0;

QY 1 HLGNVKYL 9  
Db 3 HLGNVKYL 11

## RESULT 10

Q70GK3  
ID Q70GK3 PRELIMINARY; PRT; 331 AA.  
AC Q70GK3;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Trap protein (Fragment).  
GN Name-trap;  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mamillapalli A., Joshi H., Malhotra P.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

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DR EMBL; AJ581764; CAE46492.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00092; VWA; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS50234; VWEA; 1.
FT NON TER 331
SQ SEQUENCE 331 AA; 37625 MW; 4258443729D48835 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
DB 3 HLGNVKYL 11

RESULT 13
CAE46492 PRELIMINARY; PRT; 331 AA.
AC CAE46492;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Trap protein (Fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM3-21;
RA Mamilapalli A.; Joshi H., Malhotra P.;
RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in Indian isolates."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581764; CAE46492.1; -.
FT NON TER 331
SQ SEQUENCE 331 AA; 37625 MW; 4258443729D48835 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
DB 3 HLGNVKYL 11

RESULT 14
CAE46493 PRELIMINARY; PRT; 331 AA.
AC CAE46493;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Trap protein (Fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM3-21;
RA Mamilapalli A.; Joshi H., Malhotra P.;
RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in Indian isolates."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581769; CAE46496.1; -.
FT NON TER 331
SQ SEQUENCE 331 AA; 37573 MW; 60EBBAC3FDD9C779 CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9
DB 3 HLGNVKYL 11

RESULT 12
CAE46493 PRELIMINARY; PRT; 331 AA.
AC CAE46493;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DE Trap protein (Fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM3-21;
RA Mamilapalli A.; Joshi H., Malhotra P.;
RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in Indian isolates."
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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Db 3 HLGNVKYL 11

RESULT 15

CAE46497 PRELIMINARY; PRT; 331 AA.  
 AC CAE46497;  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Trap protein (Fragment).  
 GN TRAP.  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CM3-56;  
 RA Mamilapalli A., Joshi H., Malhotra P.;  
 RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in  
 Indian isolates."  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ581770; CAE46497.1; -.  
 FT NON\_TER 331  
 SQ SEQUENCE 331 AA; 37521 MW; CBD1823A0C8C49EB CRC64;

Query Match 100.0%; Score 48; DB 2; Length 331;  
 Best Local Similarity 100.0%; Pred. No. 0.44;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9  
 Db 3 HLGNVKYL 11

Search completed: December 6, 2004, 15:30:15  
 Job time : 126.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:14:37 ; Search time 119 Seconds  
(without alignments)  
27.131 Million cell updates/sec

Title: US-10-042-202-1  
Perfect score: 48  
Sequence: 1 HLGNVKYL 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04: \*  
1: Geneseqp1980s: \*  
2: Geneseqp1990s: \*  
3: Geneseqp2000s: \*  
4: Geneseqp2001s: \*  
5: Geneseqp2002s: \*  
6: Geneseqp2003as: \*  
7: Geneseqp2003bs: \*  
8: Geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48	100.0	9	2	AAR87267 Plasmodiu
2	48	100.0	9	2	AAY10523 HLA Class
3	48	100.0	9	2	AAY03670 Amino aci
4	48	100.0	9	5	ABG80206 MHC class
5	48	100.0	9	8	ADK69145 Epitope 1
6	48	100.0	9	8	ADQ10943 Plasmodiu
7	48	100.0	15	7	ADE79950 Plasmodiu
8	48	100.0	20	5	AAQ17442 P falcipa
9	48	100.0	229	2	AAY03681 Amino aci
10	48	100.0	559	2	AAR05427 Circumspo
11	40	83.3	15	2	AAW85142 Helper T-
12	39	81.2	123	4	ABM00029 Allergen
13	39	81.2	133	2	AAR22261 P14 aller
14	39	81.2	133	2	AAR71926 Birch pol
15	39	81.2	133	2	AAY25650 Betula sp
16	39	81.2	133	6	AAE31498 Birch tre
17	39	81.2	133	7	ADC34899 Tree alle
18	38	79.2	753	4	AAW79139 Human pro
19	38	79.2	764	4	AAW80123 Human pro
20	38	79.2	1006	6	ABP98831 Human str
21	38	79.2	1006	7	ADJ95090 Novel NOV
22	37	77.1	131	6	AAE31507 Latex Hev
23	37	77.1	157	4	AAAG72436 Human OR-
24	37	77.1	157	4	AAAG72246 Human olf
25	37	77.1	265	6	ADA36329 Acinetoba

26	77.1	312	5	ABJ04042	Human G-p
27	77.1	312	8	ADH30958	Human G-p
28	77.1	338	4	AAAG71620	Human olf
29	75.0	131	6	AAE31518	Pear Pyr
30	75.0	131	6	AAE31504	Latex Hev
31	75.0	131	6	AAE31509	Latex Hev
32	75.0	131	6	AAE31506	Latex Hev
33	75.0	131	6	AAE31508	Latex Hev
34	75.0	134	2	AAW78445	O.europae
35	75.0	134	2	AAW78446	O.europae
36	75.0	134	2	AAW78440	O.europae
37	75.0	134	6	AAE31512	Olive tre
38	75.0	134	6	AAE31511	Olive tre
39	75.0	134	6	AAE31513	Olive tre
40	75.0	260	4	ABM00025	Allegren
41	75.0	432	8	ADJ49584	Oil-asoc
42	75.0	433	4	AAAG62633	C album c
43	75.0	433	4	AAAG62635	C album c
44	75.0	433	5	ABG70944	C. Album
45	75.0	433	5	ABG70942	C. Album

ALIGNMENTS

RESULT 1  
AAR87267  
ID AAR87267 standard; peptide; 9 AA.  
XX  
XX AAR87267;  
AC  
AC  
DT 16-MAY-1996 (first entry)  
DE Plasmodium falciparum HLA-A2 epitope tr26.  
XX

Thrombospondin-related anonymous protein; human leucocyte antigen; HLA; class 1; HLA-A2; epitope; malaria; vaccine; CTL induction; cytotoxic T lymphocyte; TRAP.

Plasmodium falciparum.

W09526982-A2.

12-OCT-1995.

31-MAR-1995; 95WO-GB000737.

31-MAR-1994; 94GB-00006492.

(ISIS-) ISIS INNOVATION LTD.

Hill AVS, Aidoo M, Allsopp CEM, Lalvani A, Plebanski M;

Whittle HC;

WPI; 1995-358584/46.

Plasmodium falciparum peptide(s) - useful in vaccine compositions for immunising against malaria.

Claim 1; Page 18; 23pp; English.

Two Gambian individuals showed CTL responses to HLA-A2 peptides tr26, tr29 and tr39 (AAR87267-R87269) derived from Plasmodium falciparum. Thrombospondin-related anonymous protein (TRAP). All three of these peptides bound to HLA-A2 in an assembly assay. Peptide tr39 was identified as the HLA-A2-restricted epitope. The peptides (and analogues and variants of them) are useful in vaccines against malaria

Sequence 9 AA;

Query Match 100.0%; Score 48; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9  
 Db 1 HLGNVKYL 9

## RESULT 2

AAV10523  
 ID AAY10523 standard; peptide; 9 AA.

XX AC AAY10523;

DT 12-MAY-1999 (first entry)

XX DE HLA Class I motif peptide SEQ ID NO:453.

XX KW Cytotoxic T-lymphocyte response; CTL; antigen; lymphatic system;  
 immunisation; tumour; infectious disease; immunotherapy; cancer;  
 XX KW malignant melanoma; viral disease; hepatitis; AIDS.

OS Synthetic.  
 OS Plasmodium falciparum.

XX PN WO9902183-A2.

XX PD 21-JAN-1999.

XX PF 10-JUL-1998; 98WO-US014289.

XX PR 10-JUL-1997; 97CA-02209815.

XX PR 10-DEC-1997; 97US-00988320.

XX PA (CTL-I-) CTL IMMUNOTHERAPIES CORP.

XX PI Kuendig TM, Simard JDL;

XX PS WPI; 1999-120514/10.

XX PT Inducing a cytotoxic T lymphocyte response - by maintaining a level of  
 PT antigen in the lymphatic system of a mammal so as to provide a sustained  
 PT CTL response, used to treat, e.g. AIDS.

XX PS Disclosure; Page 44; 1999p; English.

XX CC The present invention describes a method of inducing and/or sustaining an  
 CC immunological cytotoxic T lymphocyte (CTL) response in a mammal. The  
 CC method comprises: (a) delivering an antigen to the mammal at a level to  
 CC induce an immunological CTL response in the mammal; and (b) maintaining  
 CC the level of the antigen in the mammal's lymphatic system to maintain the  
 CC immunologic CTL response. The method can be used for the delivery of e.g.  
 CC a differentiation antigen, a tumour-specific multineage antigen, an  
 CC embryonic antigen, an oncogene antigen, a mutated tumour-suppressor gene  
 CC antigen, or a viral antigen. They can be used for the treatment of  
 CC disease such as cancer, e.g. malignant melanoma or infectious disease,  
 CC e.g. viral disease such as hepatitis or AIDS. Sustained antigen delivery  
 CC to the lymphatic system provides for potent CTL stimulation that takes  
 CC place in the milieu of the lymphoid organ, and it sustains stimulation  
 CC that is necessary to keep CTL active, cytotoxic and recirculating through  
 CC the body. AAY10071 to AAY10639 represent examples of peptide antigens  
 XX given in the present invention

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9  
 Db 1 HLGNVKYL 9

## RESULT 3

RESULT 4

ABG80206

AAV03670

ID AAY03670 standard; peptide; 9 AA.

XX AC AAY03670;

XX DT 07-JUN-1999 (first entry)

XX DE Amino acid sequence of the malaria (M) string CTL epitope Tr36.

XX KW CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;  
 KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;  
 KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;  
 KW melanoma; HIV; breast; colon; vaccination.

XX OS Plasmodium falciparum.

XX PN WO9856919-A2.

XX PD 17-DEC-1998.

XX PF 09-JUN-1998; 98WO-GB001681.

XX PR 09-JUN-1997; 97GB-00011957.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PI McMichael AJ, Hill AVS, Gilbert SC, Schneider J, Plebanski M;  
 PI Hanke T, Smith GL, Blanchard T;

XX DR WPI; 1999-070325/06.

XX DR N-PSDB; AAX29210.

XX PT Generating CD8-positive T cell response to target antigen using  
 PT recombinant poxvirus - for treating or preventing malaria and HIV  
 PT infection, also epitope strings from Plasmodium and HIV.

XX PS Claim 38; Page 19; 85pp; English.

XX CC The invention relates to methods and reagents for generating a protective  
 CC CD8+ T-cell immune response against at least one target antigen. The kits  
 CC of the invention comprises (i) as priming composition, a source of one or  
 CC more CD8+ T-cell cytotoxic T lymphocytes (CTL) epitopes of the target  
 CC antigen, plus a carrier and (ii) as boosting composition a source of CTL  
 CC epitopes, with at least one CTL epitope the same as used in (i), with  
 CC this source being a non-replicating or replication-impaired recombinant  
 CC poxvirus vector (PVV) plus a carrier. If the source of CTL epitopes in  
 CC (i) is a viral vector, then the vector in (ii) is from a different virus.  
 CC The kits are used to generate an immune response (prophylactic or  
 CC therapeutic) against pathogens or tumours, specifically against malaria  
 CC parasites such as P. falciparum, or HIV, and also many other bacterial,  
 CC viral or parasitic pathogens. The kits are also used for protective  
 CC response against melanoma and cancer of breast or colon, and generally  
 CC wherever a strong CD8+ response is protective. The boosting composition  
 CC may be used alone to boost a naturally primed response against malaria.  
 CC The specified PVV provide an excellent booster effect, better than that  
 CC from wild-type poxvirus, resulting in complete rather than partial  
 CC protection against sporozoite challenge. Also PVV are safer to use than  
 CC wild-type virus. Sequences AAY03661-680 represent CTL peptide epitopes of  
 CC the malaria (M) string

XX SQ Sequence 9 AA;

Query Match 100.0%; Score 48; DB 2; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HLGNVKYL 9  
 Db 1 HLGNVKYL 9

ID ABG80206 standard; peptide; 9 AA.  
XX  
AC ABG80206;  
XX  
DT 29-AUG-2003 (revised)  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE MHC class I molecule, viral epitope #454.  
XX  
XX Major histocompatibility complex; MHC; MHC class I molecule; virus;  
XX epitope; cytotoxic T lymphocyte response; CTL response; lymphatic system;  
XX antigen; immunogenic; malignant tumour; carcinoma; melanoma; leukaemia;  
XX lymphoma; infectious disease; hepatitis; malaria; measles; tuberculosis;  
XX acquired immune deficiency syndrome; AIDS.  
XX  
OS Viruses.  
XX  
XX WO200262368-A2.  
XX  
PN 15-AUG-2002.  
XX  
PD 22-JAN-2002; 2002WO-US002033.  
XX  
PF 02-FEB-2001; 2001US-00776232.  
XX  
PR (CTL-) CTL IMMUNOTHERAPIES CORP.  
XX  
PA Kundig TM, Simard JLL;  
XX  
PI WPI; 2002-657506/70.  
XX  
DR Inducing or sustaining immunological cytotoxic T lymphocyte response in a  
XX mammal, useful for treating a mammal with malignant tumor or infectious  
XX disease, by directly administering an antigen to the lymphatic system of  
XX the mammal.  
XX  
PS Disclosure; Page 37; 73pp; English.  
XX  
XX The invention relates to a method of inducing and/or sustaining an  
XX immunological cytotoxic T lymphocyte (CTL) response in a mammal  
XX comprising administering directly to the lymphatic system of the mammal:  
XX (a) an antigen in the form of a polypeptide; (b) a vector comprising a  
XX nucleic acid encoding the antigen; or (c) a non-peptide antigen. The  
XX method is useful for inducing and/or sustaining CTL response in a mammal.  
XX This is particularly useful for treating a mammal having a malignant  
XX tumour (e.g. carcinoma, melanoma, leukaemia or lymphoma) or infectious  
XX disease (e.g. hepatitis, acquired immune deficiency syndrome (AIDS),  
XX malaria, measles or tuberculosis), or in an animal having a  
XX predisposition to these diseases. The mammal may be dogs, mice,  
XX cattle, sheep, pigs, goats, rabbits, or preferably humans. ABG79753-  
XX ABG80319 represent viral epitopes on major histocompatibility complex  
XX (MHC) class I molecules, used in the method of the invention. (Updated on  
XX 29-AUG-2003 to standardise OS field)  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 48; DB 5; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Mismatches 0; Gaps 0;  
Matches 9; Conservative 0; Indels 0; Gaps 0;  
QY 1 HLGNVKYLIV 9  
Db 1 HLGNVKYLIV 9  
RESULT 5  
ADK69145  
ID ADK69145 standard; peptide; 9 AA.  
XX  
AC ADK69145;  
XX  
DT 06-MAY-2004 (first entry)  
XX

DE Epitope liberation-related peptide SeqID508.  
XX  
KW epitope liberation; substrate; proteasome; cytostatic; antibacterial;  
KW protozoacide; fungicide; T-cell activator; vaccine; housekeeping epitope;  
KW cytotoxic T lymphocyte; CTL; adoptive immunotherapy; neoplastic cell;  
KW virus; bacterium; protozoan; fungus; housekeeping proteasome system.  
XX  
OS Plasmodium falciparum.  
XX  
XX US2003228634-A1.  
XX  
PN 11-DEC-2003.  
XX  
PD 07-NOV-2002; 2002US-00292413.  
XX  
PF 07-NOV-2001; 2001US-0336968P.  
XX  
PR (SIMA/) SIMARD J J L.  
PA (DIAM/) DIAMOND D C.  
PA (QIUZ/) QIU Z.  
PA (LEIX/) LEI X.  
XX  
PI Simard JLL, Diamond DC, Qiu Z, Lei X;  
XX  
DR WPI; 2004-167209/16.  
XX  
XX Identifying polypeptide suitable for epitope e.g., housekeeping epitope,  
XX liberation by contacting substrate polypeptide comprising epitope of  
XX interest, with proteasome, and assaying for liberation of epitope.  
XX  
PS Disclosure; SEQ ID NO 508; 67pp; English.  
XX  
XX This invention relates to a novel method of identifying a polypeptide  
XX suitable for epitope liberation, including the steps of identifying an  
XX epitope of interest; providing substrate polypeptide sequence including  
XX the epitope, wherein the substrate permits processing by a proteasome;  
XX contacting the substrate with a composition including the proteasome;  
XX under conditions that support processing of the substrate by proteasome;  
XX and assaying for liberation of epitope. The invention may be useful for  
XX the development of compounds with a cytostatic, antibacterial,  
XX protozoacide or fungicide activity acting as T-cell activators. In  
XX addition, the invention may allow development of a vaccine. The invention  
XX is useful for identifying a polypeptide suitable for epitope liberation,  
XX where the epitope is a housekeeping epitope. The compositions comprising  
XX the identified housekeeping epitopes are useful in vitro in vaccine  
XX development or in the generation or expansion of cytotoxic T lymphocyte  
XX (CTL) to be used in adoptive immunotherapy. The invention is also useful  
XX for activating T-cells against neoplastic cells, and cells infected with  
XX virus, bacterium, protozoan or fungus. CTL epitopes are identified based  
XX on the knowledge that such epitopes are, in fact, produced by the  
XX housekeeping proteasome system. Once identified, these epitopes, embodied  
XX as peptides, can be used to successfully immunise or induce therapeutic  
XX CTL responses against housekeeping proteasome expressing target cells in  
XX the host. The present sequence is that of a peptide which is related to  
XX the method of the invention.  
XX  
SQ Sequence 9 AA;  
Query Match 100.0%; Score 48; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HLGNVKYLIV 9  
Db 1 HLGNVKYLIV 9  
RESULT 6  
ADQ10943  
ID ADQ10943 standard; peptide; 9 AA.  
XX  
AC ADQ10943;  
XX

DT 23-SEP-2004 (first entry)  
 DE Plasmodium falciparum T-cell epitope seqid 508.  
 XX  
 KW immunostimulant; cytostatic; vaccine; tumour-associated antigen SSX-2;  
 KW SSX-2 antigen; epitope cluster; MHC receptor peptide binding cleft;  
 KW immunogenic composition; immune response; cancer; vaccine vector;  
 KW epitope liberation; human leukocyte antigen; HLA A2-specific CTL;  
 KW cytotoxic T lymphocyte; T-cell epitope.  
 XX  
 OS Plasmodium falciparum.  
 XX  
 PN US2004132088-A1.  
 XX  
 XX 08-JUL-2004.  
 XX  
 XX 10-FEB-2004; 2004US-00777053.  
 XX  
 XX 07-NOV-2001; 2001US-0336968P.  
 PR 07-NOV-2002; 2002US-00292413.  
 XX  
 XX (SIMA/) SIMARD J J L.  
 PA (DIAM/) DIAMOND D C.  
 PA (QIUZ/) QIU Z.  
 PA (LEIX/) LEI X.  
 XX  
 PI Simard J J L, Diamond D C, Qiu Z, Lei X;  
 XX  
 XX WPI; 2004-517003/49.  
 XX  
 XX Novel nucleic acid encoding tumor-associated antigen SSX-2, useful in  
 PT inducing an immune response and in treating cancer.  
 XX  
 PS Disclosure; SEQ ID NO 508; 260pp; English.  
 XX  
 XX The invention describes an isolated nucleic acid (I) comprising a reading  
 CC frame comprising a first sequence, where the first sequence encodes one  
 CC or more segments of tumour-associated antigen SSX-2, which comprises a  
 CC sequence of 188 amino acids (SEQ ID NO: 40), where the first sequence  
 CC does not encode the complete SSX-2 antigen, and where each segment  
 CC comprises an epitope cluster, the cluster comprising or encoding at least  
 CC two amino acid sequences having a known or predicted affinity for a same  
 CC MHC receptor peptide binding cleft. Also described are: an isolated  
 CC polypeptide comprising the amino acid sequence encoded in the reading  
 CC frame; and an immunogenic composition comprising (I) or the polypeptide  
 CC of (I). (I) is a nucleic acid encoding a tumour-associated antigen SSX-2  
 CC comprising a fully defined sequence of 188 amino acids (SEQ ID NO: 40).  
 CC The nucleic acid, the encoded antigen, and composition are useful in  
 CC inducing an immune response and in treating cancer. Expression cassettes  
 CC are used in vaccine vectors. This is the amino acid sequence of a T-cell  
 CC epitope MHC ligand associated with methods, therapies and compositions  
 CC described in the invention.  
 XX  
 SQ Sequence 9 AA;  
 Query Match 100.0%; Score 48; DB 8; Length 9;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HLGNVKYL V 9  
 |||||  
 Db 1 HLGNVKYL V 9  
 |||||  
 RESULT 7  
 ADE79950  
 ID ADE79950 standard; peptide; 15 AA.  
 XX  
 AC ADE79950;  
 XX  
 XX 29-JAN-2004 (first entry)  
 XX  
 DE Plasmodium epitope #6 for method to augment CD8+ T-cell immune response.

XX  
 KW antimalarial; cytostatic; vaccine; immune response;  
 KW non-hepadnaviral antigen; hepatitis B core particle; CD8+ T-cell;  
 KW epitope; poxvirus vector; cancer; malaria; epitope.  
 XX  
 OS Plasmodium sp.  
 XX  
 PN WO2003066833-A2.  
 XX  
 PD 14-AUG-2003.  
 XX  
 XX 07-FEB-2003; 2003WO-US003897.  
 XX  
 PR 08-FEB-2002; 2002US-0354963P.  
 XX  
 PA (UYNV-) UNIV NEW YORK MEDICAL CENT.  
 XX  
 PI Zavala F, Birkett AJ;  
 XX  
 DR WPI; 2003-748124/70.  
 XX  
 XX Generating an immune response against a non-hepadnaviral antigen in a  
 PT mammal, useful for treating or preventing cancer or malaria, by  
 PT administering a priming component comprising a recombinant hepatitis B  
 PT core particle.  
 XX  
 PS Claim 57; SEQ ID NO 6; 85pp; English.  
 XX  
 XX The invention relates to a method of generating an immune response  
 CC against a non-hepadnaviral antigen in a mammal by administering (to the  
 CC mammal) at least 1 dose of a priming component comprising a recombinant  
 CC hepatitis B core particle (rHEP) (which is a carrier for 1 or more non-  
 CC hepadnaviral CD8+ T-cell epitopes of the antigen). The method may be  
 CC supplemented by the use of a boosting stage comprising a non-replicating  
 CC or replication-impaired recombinant poxvirus vector. The method is useful  
 CC for generating an immune response against a non-hepadnaviral antigen in a  
 CC mammal for treating or preventing cancer or malaria. This sequence  
 CC represents a peptide epitope from Plasmodium the causative agent for  
 CC malaria.  
 XX  
 SQ Sequence 15 AA;  
 Query Match 100.0%; Score 48; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.013;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HLGNVKYL V 9  
 |||||  
 Db 3 HLGNVKYL V 11  
 |||||  
 RESULT 8  
 AAO17442  
 ID AAO17442 standard; peptide; 20 AA.  
 XX  
 AC AAO17442;  
 XX  
 XX 11-JUL-2002 (first entry)  
 XX  
 DE P falciparum TRAP CD4+ T cell epitope #1.  
 XX  
 DE Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;  
 KW poxvirus vector; HIV; malaria; Helicobacter pylori; influenza; hepatitis;  
 KW viral infection; leprosy; protozoan parasite; cancer; tuberculosstatic;  
 KW anti-HIV; protozoicide; antibacterial; virucide; hepatotropic;  
 KW antiinflammatory; antileptotic; cytostatic; epitope.  
 XX  
 OS Plasmodium falciparum.  
 XX  
 PN WO200224224-A2.  
 XX  
 PD 28-MAR-2002.  
 XX



XX PS Disclosure; Page 7; 49pp; English.

XX CC The CS protein is produced during the merozoite stage of the malaria parasite. The CS-related protein can be used to produce vaccines. The antibodies can be used for purificn. of the polypeptides. The vector may be a recombinant virus, esp. baculovirus or the peptide can be chemically prepared. Fragments of the peptide preferably contain a conserved sequence, egsidues 244 to 291 and more particularly a polypeptide selected from the following group: A) WDEWSPCSVTCKGRSRKR B) WDEWSPCSVTCKGTR C) EWSVPCVTCGK D) PCSVTCGKG E) WSPCSVTCG See also CAAQ02049. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS field)

XX SQ Sequence 559 AA;

Query Match 100.0%; Score 48; DB 2; Length 559;  
Best Local Similarity 100.0%; Pred. No. 0.8;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HLGNVKYL V 9  
Db 3 HLGNVKYL V 11

RESULT 11  
AAW85142  
ID AAW85142 standard; peptide; 15 AA.  
AC AAW85142;  
XX 16-FEB-1999 (first entry)

DE Helper T-cell peptide derived from a TRAP protein.

XX KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;  
KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;  
KW acquired immune deficiency syndrome; malaria; cancer;  
KW allograft rejection; allergy; Lyme disease; hepatitis;  
KW post-streptococcal endocarditis; glomerulonephritis;  
KW food hypersensitivity.

XX OS Synthetic.  
OS Plasmodium falciparum.

XX PN WO9832456-A1.  
XX 30-JUL-1998.

XX PF 23-JAN-1998; 98WO-US001373.  
XX 23-JAN-1997; 97US-0036713P.  
XX 07-FEB-1997; 97US-0037432P.  
XX (EPIM-) EPIMMUNE INC.

XX PI Sette A, Sidney J, Southwood S;  
XX WPI; 1998-427679/36.

XX PT Composition containing peptide that induces cytotoxic T lymphocyte response, and helper peptide - can bind to human leucocyte antigen alleles, used to treat or prevent cancers, parasitic infections and autoimmune disease.

XX PS Claim 11; Page 37; 51pp; English.

XX CC AAW85138-283 represent helper T-cell peptides, which can bind to the human leucocyte antigens (HLA) DR4w4, DR1 and DR7. The peptides are used in the course of the invention. The specification describes peptides that induce a cytotoxic T lymphocyte (CTL) response, and T-helper peptides, that are used together to generate a CTL response for the

CC treatment or prevention of viral, fungal, bacterial or parasitic infections (e.g. hepatitis, acquired immune deficiency syndrome or malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate cancer or condyloma acuminatum). Helper T-cell peptides may be used alone to induce a helper T cell response, e.g. in cases of autoimmune disease, allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal endocarditis, glomerulonephritis and food hypersensitivity

XX SQ Sequence 15 AA;

Query Match 83.3%; Score 40; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.54;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 LGNVKYL V 9  
Db 1 LGNVKYL V 8

RESULT 12  
ABM00029  
ID ABM00029 standard; protein; 123 AA.  
XX AC ABM00029;  
XX 02-APR-2003 (first entry)

DE Allergen profilin-birchpollen SEQ ID NO 20.

XX KW Allergen; protein coordinate data; vaccine; antiallergic; immunogenicity;  
KW detergent; personal care composition; cosmetic.

XX OS Unidentified.

XX PN WO200183559-A2.  
XX 08-NOV-2001.  
XX 30-APR-2001; 2001WO-DK000293.  
XX 28-APR-2000; 2000DK-00000707.  
XX 10-MAY-2000; 2000US-0203345P.  
XX 28-FEB-2001; 2001DK-00000327.  
XX 21-MAR-2001; 2001US-0277817P.  
XX (NOVO ) NOVOZYMES AS.

XX PI Roggen EL, Ernst S, Svendsen A, Friis EP, Von Der Osten C;  
XX WPI; 2001-626552/72.

XX PT Selecting protein variants having modified immunogenicity, used to produce vaccines, detergents and personal care compositions, involves localizing epitope sequences on the three-dimensional structure of a protein.

XX PS Claim 67; Page 495; 513pp; English.

XX CC The invention relates to selecting a protein variant having modified immunogenicity, compared to a parent protein, comprising using the antibody binding sequence to localise epitope sequences on the three dimensional structure of the parent protein and defining an epitope area including amino acids within 5 Angstrom of the epitope amino acids. The method is useful for identifying structural epitopes on the 3-dimensional surface of commercial and environmental allergens. Compositions containing the protein variants are used as vaccines, detergents and personal care compositions, e.g. shampoo, balsam, hair conditioners, hair waving compositions, hair dyeing compositions, hair tonic, hair liquid, hair cream, hair rinse, hair spray, chewing gum, skin cream, sunscreen, shaving foam, cream soap, skin milk or foundation. The present sequence is that of a polypeptide of the invention

XX SQ Sequence 123 AA;



Query Match 81.2%; Score 39; DB 4; Length 123;  
 Best Local Similarity 66.7%; Pred. No. 9.3;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9  
 ||| :|||  
 Db 58 HLGGIKYM 66

RESULT 13  
 AAR22261  
 ID AAR22261 standard; protein; 133 AA.  
 AC AAR22261;  
 XX  
 XX 24-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 09-JUL-1992 (first entry)  
 XX  
 DE P14 allergen of birch.  
 XX  
 KW Epitopes; pollen; food allergy; IgE antibodies; hyposensitisation.  
 XX  
 OS Betula pendula.  
 PN WO9203551-A.  
 XX  
 PD 05-MAR-1992.  
 XX  
 XX 09-AUG-1991; 91WO-EP001513.  
 PF  
 XX 13-AUG-1990; 90AT-00001685.  
 PR 11-APR-1991; 91US-00683832.  
 DR N-PSDB; AAQ22352.  
 XX  
 PA (BIOM-) BIOWAY BIOTECH PROD.  
 XX  
 XX Valenta R, Uche, Duchene M, Pettenburg K, Breitenbac M, Kraft D;  
 PI Rumpold H, Scheiner O;  
 XX  
 XX WPI; 1992-096895/12.  
 DR N-PSDB; AAQ22352.  
 XX  
 PT Recombinant DNA encoding polypeptide with epitope(s) of P14 allergens -  
 PT for treatment and diagnosis of pollen or food allergy, and for purificn.  
 PT of P14 allergens.  
 XX  
 PS Disclosure; Fig 4; 68pp; English.  
 XX  
 CC The protein sequence was deduced from the cDNA encoding the P14 allergen  
 CC from birch obtd. by screening a cDNA library constructed from birch  
 CC pollen. The full length gene for P14 was expressed in pK223-3, encoding  
 CC a protein of 133 amino acids. The protein can be used to immunologically  
 CC detect IgE antibodies in serum to diagnose allergies, allowing for  
 CC hyposensitisation therapy of people with pollen or food allergies, and to  
 CC detect allergic reactions to P14. See also AAR22260. (Updated on 25-MAR-  
 CC 2003 to correct PF field.) (Updated on 24-OCT-2003 to standardise OS  
 CC field)  
 XX  
 SQ Sequence 133 AA;

Query Match 81.2%; Score 39; DB 2; Length 133;  
 Best Local Similarity 66.7%; Pred. No. 10;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9  
 ||| :|||  
 Db 68 HLGGIKYM 76

RESULT 15  
 AAY25650  
 ID AAY25650 standard; protein; 133 AA.  
 XX  
 AC AAY25650;  
 XX  
 XX 30-SEP-1999 (first entry)  
 DT  
 DE Betula sp. allergen 130975 Bet v 2 protein fragment.  
 XX  
 KW Major histocompatibility complex; class II; desensitising; human;  
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;  
 KW chitomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;  
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;  
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;  
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.  
 XX  
 OS Betula sp.

XX AAR71926;  
 AC  
 XX 16-OCT-2003 (revised)  
 DT 09-NOV-1995 (first entry)  
 XX  
 DE Birch pollen P14 allergen.  
 XX  
 KW Birch tree pollen allergen; P14 protein; pollinosis; profilin;  
 KW in vitro diagnosis; antigenicity; poly L-proline; affinity.  
 XX  
 OS Betula pendula.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 114..133  
 FT /label= epitope  
 FT /note= "when coupled to beta-galactosidase, this peptide  
 FT represents an IgE-binding epitope"  
 XX  
 PN AT9400740-A.  
 XX  
 PD 15-FEB-1995.  
 XX  
 PF 13-AUG-1990; 94AT-00000740.  
 XX  
 PR 13-AUG-1990; 94AT-00000740.  
 XX  
 PA (BIOM-) BIOWAY BIOTECHNIK PROD & HANDELS GMBH.  
 XX  
 DR WPI; 1995-115733/16.  
 DR N-PSDB; AAQ89191.  
 XX  
 PT Use of poly(L-proline) in in vitro diagnosis of P14 birch allergen. - as  
 PT substitute for antibody, also for allergen purification and recovery from  
 PT pollen extract.  
 XX  
 PS Claim 1; Fig 4; 38pp; German.  
 XX  
 CC The birch pollen allergen protein P14 (AAR71926) is encoded by the cDNA  
 CC sequence AAQ89191. The allergen has affinity for poly(L-proline); the use  
 CC of poly(L-proline) for affinity purification or for in vitro diagnosis of  
 CC P14 and highly similar proteins is claimed. (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 133 AA;

Query Match 81.2%; Score 39; DB 2; Length 133;  
 Best Local Similarity 66.7%; Pred. No. 10;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 HLGNVKYL 9  
 ||| :|||  
 Db 68 HLGGIKYM 76

RESULT 15  
 AAY25650  
 ID AAY25650 standard; protein; 133 AA.  
 XX  
 AC AAY25650;  
 XX  
 XX 30-SEP-1999 (first entry)  
 DT  
 DE Betula sp. allergen 130975 Bet v 2 protein fragment.  
 XX  
 KW Major histocompatibility complex; class II; desensitising; human;  
 KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;  
 KW chitomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;  
 KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;  
 KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;  
 KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity.  
 XX  
 OS Betula sp.

XX WO9934826-A1.  
XX  
XX PD 15-JUL-1999.  
XX  
XX PF 11-JAN-1999; 99WO-GB0000080.  
XX  
XX PR 09-JAN-1998; 98GB-00000445.  
XX PR 21-SEP-1998; 98GB-00020474.  
XX  
XX PA (INCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
XX  
XX PI Larche M, Kay AB;  
XX WPI; 1999-458255/38.  
XX  
XX Desensitizing patients to polypeptide allergens.  
XX  
XX Example 6; Page 69; 117pp; English.  
XX  
XX This invention describes a novel method of desensitizing a patient to a  
XX polypeptide allergen and comprises administering to the patient a peptide  
XX derived from the allergen where restriction to a MHC Class II molecule  
XX possessed by the patient can be demonstrated for the peptide and the  
XX peptide is able to induce a late phase response in an individual who  
XX possesses the MHC Class II molecule. The methods can be used for  
XX desensitizing patients to allergens present in e.g. grass, tree and weed  
XX (including ragweed) pollens, fungi and moulds, foods, stinging insects,  
XX the chiromidae (non-biting midges), spiders and mites, housefly, fruit  
XX fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,  
XX non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of  
XX Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,  
XX sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to  
XX produce immunological vaccines which may be used to prevent and/or treat  
XX conditions involving hypersensitivity to allergens. This sequence  
XX represents a birch (Betula sp.) allergen 114922 Bet v 2  
XX  
SQ Sequence 133 AA;  
Query Match 81.2%; Score 39; DB 2; Length 133;  
Best Local Similarity 66.7%; Pred. No. 10;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 HLGNNKYL 9  
DB 68 HLGGIKYM 76

Search completed: December 6, 2004, 15:26:06  
Job time : 131 secs

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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:14:37 ; Search time 119 seconds  
(without alignments)  
27.131 Million cell updates/sec

Title: US-10-042-202-17  
Perfect score: 42  
Sequence: 1 KNKEKALII 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04 : \*  
1: Geneseqp1980s : \*  
2: Geneseqp1990s : \*  
3: Geneseqp2000s : \*  
4: Geneseqp2001s : \*  
5: Geneseqp2002s : \*  
6: Geneseqp2003as : \*  
7: Geneseqp2003bs : \*  
8: Geneseqp2004s : \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	2 AAR87283	Aar87283 Plasmodiu
2	42	100.0	9	7 ADE79963	Ade79963 Plasmodiu
3	42	100.0	11	2 AAY03664	Aay03664 Amino aci
4	42	100.0	229	2 AAY03681	Aay03681 Amino aci
5	42	100.0	559	2 AAR05427	Aar05427 Circumpo
6	39	92.9	348	6 ADA48468	Ada48468 Rice prot
7	38	90.5	177	5 ABB47928	Abb47928 Listeria
8	35	83.3	227	5 ABP40575	Abp40575 Staphyloc
9	34	81.0	9	2 AAR87282	Aar87282 Plasmodiu
10	34	81.0	9	7 ADE79962	Ade79962 Plasmodiu
11	34	81.0	224	7 ABO68759	Abo68759 Pseudomon
12	34	81.0	467	5 ABP38607	Abp38607 Staphyloc
13	33	78.6	102	8 ADM87702	Adm87702 Human EST
14	33	78.6	171	6 ABM70065	Abm70065 Phototrab
15	33	78.6	181	7 ABO64995	Abo64995 Klebsiell
16	33	78.6	303	8 ADJ66998	Adj66998 Human sec
17	33	78.6	369	8 ADM87247	Adm87247 Human pro
18	33	78.6	440	3 AAG15384	Aag15384 Arabidops
19	33	78.6	459	3 AAG15383	Aag15383 Arabidops
20	32	76.2	119	5 ABU51874	Abu51874 Helicobac
21	32	76.2	137	6 ABU40414	Abu40414 Protein e
22	32	76.2	142	3 AAG38716	Aag38716 Arabidops
23	32	76.2	142	3 AAG22006	Aag22006 Arabidops
24	32	76.2	159	5 ABU51129	Abu51129 Helicobac
25	32	76.2	164	3 AAG38715	Aag38715 Arabidops

## ALIGNMENTS

## RESULT 1

AAR87283  
ID AAR87283 standard; peptide; 9 AA.

XX  
AC AAR87283;

DT 16-MAY-1996 (first entry)

DE Plasmodium falciparum HLA-B8 restricted epitope tr43.

XX  
KW Thrombospondin-related anonymous protein; human leucocyte antigen; HLA; class I; HLA-B8; epitope; malaria; vaccine; CTL induction; cytotoxic T lymphocyte; TRAP.

XX  
OS Plasmodium falciparum.

XX  
PN WO9526982-A2.

XX  
PD 12-OCT-1995.

PF 31-MAR-1995; 95WO-GB000737.

XX  
PR 31-MAR-1994; 94GB-00006492.

XX  
(ISIS-) ISIS INNOVATION LTD.

XX  
PI Hill AVS, Aidoo M, Allsopp CEM, Lalvani A, Plebanski M;

XX  
PI Whittle HC;

XX  
WPI; 1995-358584/46.

XX  
PT Plasmodium falciparum peptide(s) - useful in vaccine compositions for immunising against malaria.

XX  
Claim 1; Page 18; 23pp; English.

XX  
CC Cytotoxic T lymphocytes from malaria-exposed Gambian individuals with HLA-B8 showed significant lysis of a pool of the four peptides tr42, tr43, tr44 and tr45 (all derived from Plasmodium falciparum thrombospondin-related anonymous protein (TRAP)). The peptides tr42 and tr43 (AAR87282 and AAR87283) bound to HLA-B8 in the HLA assembly assay. Subsequently, the same CTL line showed specific lysis of tr42 only, while CTL from another adult showed specific lysis of the tr43 peptide, identifying tr42 and tr43 as overlapping HLA-B8 restricted epitopes. These peptides will be useful in a malaria vaccine

XX  
SQ Sequence 9 AA;

Aag22005 Arabidops  
Adc97603 B. faeciu  
Aaw27941 Staphyloc  
Aag22004 Arabidops  
Aag38714 Arabidops  
Abu50835 Helicobac  
Aaw20722 H. pylori  
Abu51739 Helicobac  
Aar64140 Heymann n  
Abu51761 Helicobac  
Abu51349 Helicobac  
Aau35694 Helicobac  
Abu30690 Protein e  
Abu17482 Protein e  
Abu24333 Protein e  
Abu23836 Protein e  
Abu51958 Helicobac  
Aaw14068 Helicobac  
Aab46319 H. pylori  
Aay35710 Chlamydia

26 32 76.2 164 3 AAG22005  
27 32 76.2 166 7 ADC97603  
28 32 76.2 167 2 AAW27941  
29 32 76.2 168 3 AAG22004  
30 32 76.2 168 3 AAG38714  
31 32 76.2 179 5 ABU50835  
32 32 76.2 234 2 AAW20722  
33 32 76.2 264 5 ABU51739  
34 32 76.2 269 2 AAR64140  
35 32 76.2 287 5 ABU51761  
36 32 76.2 314 5 ABU51349  
37 32 76.2 352 4 AAU35694  
38 32 76.2 352 6 ABU30690  
39 32 76.2 355 6 ABU17482  
40 32 76.2 358 6 ABU24333  
41 32 76.2 359 6 ABU23836  
42 32 76.2 440 5 ABU51958  
43 32 76.2 732 2 AAW14068  
44 32 76.2 733 4 AAB46319  
45 32 76.2 810 2 AAY35710

Query Match 100.0%; Score 42; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 1 KNKEKALII 9

RESULT 2  
ADE79963  
ID ADE79963 standard; peptide; 9 AA.  
XX  
AC ADE79963;  
XX  
XX 29-JAN-2004 (first entry)  
XX  
XX Plasmodium epitope #19 for method to augment CD8+ T-cell immune response.  
XX  
XX antimalarial; cytostatic; vaccine; immune response;  
KW non-hepadnaviral antigen; hepatitis B core particle; CD8+ T-cell;  
KW epitope; poxvirus vector; cancer; malaria; epitope.  
XX  
XX Plasmodium sp.  
XX  
XX WO2003066833-A2.  
XX  
XX 14-AUG-2003.  
XX  
XX 07-FEB-2003; 2003WO-US003897.  
XX  
XX 08-FEB-2002; 2002US-0354963P.  
XX  
XX (UUNY-) UNIV NEW YORK MEDICAL CENT.  
XX  
XX Zavala F, Birkett AJ;  
XX  
XX WPI; 2003-748124/70.  
XX  
XX Generating an immune response against a non-hepadnaviral antigen in a  
PT mammal, useful for treating or preventing cancer or malaria, by  
PT administering a priming component comprising a recombinant hepatitis B  
PT core particle.  
XX  
XX Claim 57; SEQ ID NO 19; 85pp; English.  
XX  
XX The invention relates to a method of generating an immune response  
CC against a non-hepadnaviral antigen in a mammal by administering (to the  
CC mammal) at least 1 dose of a priming component comprising a recombinant  
CC hepatitis B core particle (rHEP) (which is a carrier for 1 or more non-  
CC hepadnaviral CD8+ T-cell epitopes of the antigen). The method may be  
CC supplemented by the use of a boosting stage comprising a non-replicating  
CC or replication-impaired recombinant poxvirus vector. The method is useful  
CC for generating an immune response against a non-hepadnaviral antigen in a  
CC mammal for treating or preventing cancer or malaria. This sequence  
CC represents a peptide epitope from Plasmodium the causative agent for  
CC malaria.  
XX  
XX Sequence 9 AA;  
SQ

Query Match 100.0%; Score 42; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 1 KNKEKALII 9

RESULT 3  
AA03664  
ID AA03664 standard; peptide; 11 AA.  
XX  
XX

AC AAY03664;  
XX  
XX 07-JUN-1999 (first entry)  
XX  
XX Amino acid sequence of the malaria (M) string CTL epitope Tr42/43.  
XX  
XX CD8+ T-cell; immune response; antigen; priming composition; CTL; epitope;  
KW cytotoxic T lymphocyte; boosting; poxvirus vector; PVV; pathogen; tumour;  
KW malaria; parasite; P. falciparum; viral; bacterial; parasitic; cancer;  
XX melanoma; HIV; breast; colon; vaccination.  
XX  
XX Plasmodium falciparum.  
XX  
XX WO9856919-A2.  
XX  
XX 17-DEC-1998.  
XX  
XX 09-JUN-1998; 98WO-GB001681.  
XX  
XX 09-JUN-1997; 97GB-00011957.  
XX  
XX (ISIS-) ISIS INNOVATION LTD.  
XX  
XX McMichael AJ, Hill AVS, Gilbert SC, Schneider J, Plebanski M;  
PI Hanke T, Smith GL, Blanchard T;  
PI  
XX WPI; 1999-070325/06.  
XX  
XX N-PSDB; AAX29204.  
XX  
XX Generating CD8-positive T cell response to target antigen using  
PT recombinant poxvirus - for treating or preventing malaria and HIV  
PT infection, also epitope strings from Plasmodium and HIV.  
XX  
XX Claim 38; Page 18; 85pp; English.  
XX  
XX The invention relates to methods and reagents for generating a protective  
CC CD8+ T-cell immune response against at least one target antigen. The kits  
CC of the invention comprises (i) as priming composition, a source of one or  
CC more CD8+ T-cell cytotoxic T lymphocytes-(CTL) epitopes of the target  
CC antigen, plus a carrier and (ii) as boosting composition a source of CTL  
CC epitopes, with at least one CTL epitope the same as used in (i), with  
CC this source being a non-replicating or replication-impaired recombinant  
CC poxvirus vector (PVV) plus a carrier. If the source of CTL epitopes in  
CC (i) is a viral vector, then the vector in (ii) is from a different virus.  
CC The kits are used to generate an immune response (prophylactic or  
CC therapeutic) against pathogens or tumours, specifically against malaria  
CC parasites such as P. falciparum, or HIV, and also many other bacterial,  
CC viral or parasitic pathogens. The kits are also used for protective  
CC response against melanoma and cancer of breast or colon, and generally  
CC wherever a strong CD8+ response is protective. The boosting composition  
CC may be used alone to boost a naturally primed response against malaria.  
CC The specified PVV provide an excellent booster effect, better than that  
CC from wild-type poxvirus, resulting in complete rather than partial  
CC protection against sporozoite challenge. Also PVV are safer to use than  
CC wild-type virus. Sequences AAY03661-680 represent CTL peptide epitopes of  
CC the malaria (M) string  
XX  
XX Sequence 11 AA;  
SQ

Query Match 100.0%; Score 42; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 3 KNKEKALII 11

RESULT 4  
AAY03681  
ID AAY03681 standard; protein; 229 AA.  
XX  
XX  
AC AAY03681;

DT	26-JUL-1990 (first entry)
XX	Circumsporozoite (CS)-related protein.
DE	Plasmodium falciparum; malaria; vaccine; ss.
KW	Plasmodium falciparum; T.9/96.
XX	Plasmodium falciparum; T.9/96.
OS	WO9001496-A.
PN	22-FEB-1990.
PD	04-AUG-1989; 89WO-GB000895.
XX	12-AUG-1988; 88GB-00019209.
PF	(REEX-) RES EXPLOITATION LTD.
XX	(THRE-) 3I RES EXPL LTD.
XX	Robson KJ, Hall JR;
PI	WPI; 1990-083478/11.
DR	N-PSDB; AAQ02047.
XX	DNA cloned from Plasmodium falciparum - used to prepare polypeptide(s) used in vaccines for persons suffering from or at risk from malaria.
PT	Disclosure; Page ?; 49pp; English.
PS	The CS protein is produced during the merozoite stage of the malaria parasite. The CS-related protein can be used to produce vaccines. The antibodies can be used for purificn. of the polypeptides. The vector may be a recombinant virus, esp. baculovirus or the peptide can be chemically prepared. Fragments of the peptide preferably contain a conserved sequence, egresidues 244 to 231 and more particularly a polypeptide selected from the following group: A) WDEMSPCSVTCGKRSRRR B) WDEMSPCSVTCGKTR C) EWSPCVTCGKG D) PCSVTCGKG E) WSPCSVTCG See also AAQ02049. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 24-OCT-2003 to standardise OS field)
CC	field)
XX	SQ Sequence 559 AA;
	Query Match 100.0%; Score 42; DB 2; Length 559;
	Best Local Similarity 100.0%; Pred. No. 11;
	Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 KNKEKALII 9 
Db	109 KNKEKALII 117
RESULT 6	
ADA48468	ID ADA48468 standard; protein; 348 AA.
XX	ADA48468;
AC	
XX	20-NOV-2003 (first entry)
DT	Rice protein conferring disease resistance in plants.
XX	disease resistance; pathogen tolerance; plant pathogen; plant; rice.
KW	Oryza sativa.
OS	WO2003000906-A2.
XX	03-JAN-2003.
PN	21-JUN-2002; 2002WO-IB002453.
PD	22-JUN-2001; 2001US-0300112P.
XX	
PR	

PR 26-SEP-2001; 2001US-0352277P.  
PR 22-MAR-2002; 2002US-036535P.  
XX  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Glazebrook J, Briggs S, Cooper B, Goff SA, Moughamer T;  
PI Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;  
XX  
XX WPI; 2003-184052/18.  
DR N-PSDB; ADA48467.  
XX  
XX New polynucleotide comprising a plant nucleotide sequence having an open  
PT reading frame that encodes a polypeptide associated with disease  
PT resistance, useful for conferring resistance or tolerance to a plant  
PT pathogen.  
XX  
PS Claim 10; SEQ ID NO 538; 299pp; English.  
XX  
CC The invention relates to a novel isolated polynucleotide comprising a  
CC plant nucleotide sequence having an open reading frame that encodes a  
CC polypeptide associated with disease resistance or its fragment having  
CC substantially the same activity as the full-length polypeptide. The  
CC polynucleotide of the invention is useful for conferring resistance or  
CC tolerance to a plant pathogen. The present sequence represents a protein  
CC conferring disease resistance used in the invention.  
XX  
SQ Sequence 348 AA;  
Query Match 92.9%; Score 39; DB 6; Length 348;  
Best Local Similarity 77.8%; Pred. No. 26;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KNKEKALII 9  
Db 311 KNKEKALLV 319  
|||||:::  
RESULT 7  
ID ABB47928 standard; protein; 177 AA.  
XX  
XX ABB47928;  
XX  
XX 05-FEB-2002 (first entry)  
XX  
XX Listeria monocytogenes protein #632.  
XX  
XX Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;  
XX vitamin B12; bacterial infection; disease.  
XX  
XX Listeria monocytogenes.  
XX  
XX WO200177335-A2.  
XX  
XX 18-OCT-2001.  
XX  
XX 11-APR-2001; 2001WO-FR001118.  
XX  
XX 11-APR-2000; 2000FR-00004629.  
XX  
XX (INSP ) INST PASTEUR.  
XX  
XX Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;  
PI Duesurget O, Chetoui F, Nedjari H, Glaser P, Kunst F, Cossart P;  
PI Daniels J, Goebel W, Krieff J, Kuhn M, Ng E, Vazquez-Boland JA;  
PI Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;  
PI Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L;  
PI Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;  
PI Maduenio E, De Pablos B, Wehlend J, Kaerst U, Entian K, Hauf J;  
PI Rose M, Voss H;  
XX  
XX WPI; 2002-010914/01.  
XX  
XX  
PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment  
PT and prevention of Listeria and related bacterial infections, and related  
PT polypeptides.  
XX  
PS Claim 6; SEQ ID NO 633; 192pp; French.  
XX  
CC The present invention relates to the genome sequence of Listeria  
CC monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of  
CC it are useful for selecting probes and primers for detecting genes in L.  
CC monocytogenes and related organisms, and for studying genetic  
CC polymorphisms and other genomes. The present sequence is a protein  
CC encoded by the genome sequence of the present invention. Proteins  
CC expressed from the genome sequence are useful for raising specific  
CC antibodies, identification of L. monocytogenes and related organisms, and  
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin  
CC B12. The genome sequence and proteins encoded by it are also useful for  
CC selecting compounds that regulate gene expression and cell replication  
CC and modulate L. monocytogenes-related diseases. In addition, the genome  
CC sequence and proteins encoded by it are useful in pharmaceutical and  
CC vaccines compositions for the treatment or prevention of infections by L.  
CC monocytogenes and related organisms. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 177 AA;  
Query Match 90.5%; Score 38; DB 5; Length 177;  
Best Local Similarity 88.9%; Pred. No. 21;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KNKEKALII 9  
Db 12 KNKEKVLII 20  
|||||:::  
RESULT 8  
ID ABP40575 standard; protein; 227 AA.  
XX  
XX ABP40575;  
XX  
XX 24-JUL-2002 (first entry)  
XX  
XX Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5420.  
XX  
XX Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
XX antibacterial; gene therapy.  
XX  
XX Staphylococcus epidermidis.  
XX  
XX US6380370-B1.  
XX  
XX 30-APR-2002.  
XX  
XX 13-AUG-1998; 98US-00134001.  
XX  
XX 14-AUG-1997; 97US-0055779P.  
XX  
XX 08-NOV-1997; 97US-0064964P.  
XX  
XX (GENO-) GENOME THERAPEUTICS CORP.  
XX  
XX Doucette-Stamm LA, Bush D;  
XX WPI; 2002-381255/41.  
XX N-PSDB; ABB93120.  
XX  
XX Novel isolated nucleic acid encoding a Staphylococcus epidermis  
PT polypeptide, useful for diagnosing and treating bacterial infections.  
XX  
XX Disclosure; SEQ ID NO 5420; 267pp; English.  
XX  
XX ABB90538 to ABB93374 represent Staphylococcus epidermidis open reading  
XX

CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
CC given in ABP35124 to ABP37960. The S. epidermidis sequences have  
CC antibacterial activity and can be used in gene therapy. The sequences can  
CC also be used in the diagnosis and treatment of bacterial infections,  
CC particularly S. epidermidis infections. The sequences can be used to  
CC screen for compounds able to interfere with the S. epidermidis life cycle  
CC or inhibit S. epidermidis infection. N.B. The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from the USPTO web site  
XX  
SQ Sequence 227 AA;

Query Match 83.3%; Score 35; DB 5; Length 227;  
Best Local Similarity 75.0%; Pred. No. 1e+02;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 NKEKALII 9  
Db 11 NKEKALV 18

RESULT 9  
AAR87282  
ID AAR87282 standard; peptide; 9 AA.

XX  
AC AAR87282;

XX  
DT 16-MAY-1996 (first entry)

XX  
DE Plasmodium falciparum HLA-B8 restricted epitope tr42.

XX  
KW Thrombospondin-related anonymous protein; human leucocyte antigen; HLA;  
KW class 1; HLA-B8; epitope; malaria; vaccine; CTL induction;  
KW cytotoxic T lymphocyte; TRAP.

XX  
OS Plasmodium falciparum.

XX  
PN WO9526982-A2.

XX  
PD 12-OCT-1995.

XX  
PF 31-MAR-1995; 95WO-GB000737.

XX  
PR 31-MAR-1994; 94GB-00006492.

XX  
PA (ISIS-) ISIS INNOVATION LTD.

XX  
PI Hill AVS, Aidoo M, Allsopp CEM, Lalvani A, Plebanski M;  
PI Whittle HC;

XX  
DR WPI; 1995-358584/46.

XX  
PT Plasmodium falciparum peptide(s) - useful in vaccine compositions for  
PT immunising against malaria.

XX  
PS Claim 1; Page 18; 23pp; English.

XX  
CC Cytotoxic T lymphocytes from malaria-exposed Gambian individuals with HLA  
CC -B8 showed significant lysis of a pool of the four peptides tr42, tr43,  
CC tr44 and tr45 (all derived from Plasmodium falciparum thrombospondin-  
CC related anonymous protein (TRAP)). The peptides tr42 and tr43 (AAR87282  
CC and AAR87283) bound to HLA-B8 in the HLA assembly assay. Subsequently,  
CC the same CTL line showed specific lysis of tr42 only, while CTL from  
CC another adult showed specific lysis of the tr43 peptide, identifying tr42  
CC and tr43 as overlapping HLA-B8 restricted epitopes. These peptides will  
CC be useful in a malaria vaccine  
XX

XX  
SQ Sequence 9 AA;

Query Match 81.0%; Score 34; DB 2; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXKEKAL 7  
Db 3 KXKEKAL 9

RESULT 10  
ADE79962

ID ADE79962 standard; peptide; 9 AA.

XX  
AC ADE79962;

XX  
DT 29-JAN-2004 (first entry)

XX  
DE Plasmodium epitope #18 for method to augment CD8+ T-cell immune response.

XX  
KW antimalarial; cytostatic; vaccine; immune response;  
KW non-hepadnaviral antigen; hepatitis B core particle; CD8+ T-cell;  
KW epitope; poxvirus vector; cancer; malaria; epitope.

XX  
OS Plasmodium sp.

XX  
PN WO2003066833-A2.

XX  
PD 14-AUG-2003.

XX  
PF 07-FEB-2003; 2003WO-US003897.

XX  
PR 08-FEB-2002; 2002US-0354963P.

XX  
PA (UYNY-) UNIV NEW YORK MEDICAL CENT.

XX  
PI Zavala F, Birkett AJ;

XX  
DR WPI; 2003-748124/70.

XX  
PT Generating an immune response against a non-hepadnaviral antigen in a  
PT mammal, useful for treating or preventing cancer or malaria, by  
PT administering a priming component comprising a recombinant hepatitis B  
PT core particle.

XX  
PS Claim 57; SEQ ID NO 18; 85pp; English.

XX  
CC The invention relates to a method of generating an immune response  
CC against a non-hepadnaviral antigen in a mammal by administering (to the  
CC mammal) at least 1 dose of a priming component comprising a recombinant  
CC hepatitis B core particle (rHEP) (which is a carrier for 1 or more non-  
CC hepadnaviral CD8+ T-cell epitopes of the antigen). The method may be  
CC supplemented by the use of a boosting stage comprising a non-replicating  
CC or replication-impaired recombinant poxvirus vector. The method is useful  
CC for generating an immune response against a non-hepadnaviral antigen in a  
CC mammal for treating or preventing cancer or malaria. This sequence  
CC represents a peptide epitope from Plasmodium the causative agent for  
CC malaria.

XX  
SQ Sequence 9 AA;

Query Match 81.0%; Score 34; DB 7; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.7e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KXKEKAL 7  
Db 3 KXKEKAL 9

RESULT 11  
ABO68759

ID ABO68759 standard; protein; 224 AA.

XX  
AC ABO68759;

XX  
DT 29-JUL-2004 (first entry)

DE Pseudomonas aeruginosa polypeptide #934.  
 XX Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.  
 KW Pseudomonas aeruginosa.  
 OS Pseudomonas aeruginosa.  
 XX US6551795-B1.  
 PN 22-APR-2003.  
 XX 18-FEB-1999; 99US-00252991.  
 XX 18-FEB-1998; 98US-0074788P.  
 PR 27-JUL-1998; 98US-0094190P.  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA Rubenfield MJ, Nolling J, Deloughery C, Bush D;  
 PI WPI; 2003-615309/58.  
 XX N-PSDB; ABD02330.  
 DR Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,  
 XX useful as molecular targets for diagnostics, prophylaxis and treatment of  
 PT pathological conditions resulting from bacterial infection.  
 XX Disclosure; SEQ ID NO 17505; 455pp; English.  
 PS The invention relates to Pseudomonas aeruginosa polypeptides and the  
 XX polynucleotides encoding them. The sequences are useful in diagnosis and  
 CC therapy of pathological conditions, as molecular targets for diagnostics,  
 CC prophylaxis and treatment of pathological conditions resulting from a  
 CC bacterial infection, for evaluating a compound, such as a polypeptide,  
 CC for the ability to bind a P. aeruginosa nucleic acid, as components of  
 CC effective antibacterial targets, as targets for antibacterial drugs,  
 CC including anti-P. aeruginosa drugs, as templates for recombinant  
 CC production of P. aeruginosa-derived peptides or polypeptides, as target  
 CC components for diagnosis and/or treatment of P. aeruginosa-caused  
 CC infection, and in detection of P. aeruginosa sequences or other sequences  
 CC of Pseudomonas species using biochip technology. Sequences AB067826-  
 CC AB084396 represent P. aeruginosa polypeptides of the invention. Note: The  
 CC sequence data for this patent did not form part of the printed  
 CC specification but was obtained in electronic format from USPTO at  
 CC seqdata.uspto.gov/sequence.html  
 XX Sequence 224 AA;  
 SQ Query Match 81.0%; Score 34; DB 7; Length 224;  
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;  
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KNKEKALI 8  
 Db 129 KNKOKALV 136  
 |||||  
 |||||  
 RESULT 12  
 ABP38607  
 ID ABP38607 standard; protein; 467 AA.  
 AC ABP38607;  
 XX 24-JUL-2002 (first entry)  
 DT Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3452.  
 DE Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;  
 XX antibacterial; gene therapy.  
 KW Staphylococcus epidermidis.  
 XX US6380370-B1.  
 PN Tang YT, Yang Y, Wang G, Zhang J, Ren F, Xue A, Wang J;  
 XX

PD 30-APR-2002.  
 XX 13-AUG-1998; 98US-00134001.  
 PF 14-AUG-1997; 97US-0055779P.  
 PR 08-NOV-1997; 97US-0064964P.  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA Doucette-Stamm LA, Bush D;  
 PI WPI; 2002-381255/41.  
 XX N-PSDB; ABN91152.  
 DR Novel isolated nucleic acid encoding a Staphylococcus epidermis  
 PT polypeptide, useful for diagnosing and treating bacterial infections.  
 XX Disclosure; SEQ ID NO 3452; 267pp; English.  
 PS ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading  
 CC frame (ORF) nucleic acid sequences which encode the amino acid sequences  
 CC given in ABP3124 to ABP37960. The S. epidermidis sequences have  
 CC antibacterial activity and can be used in gene therapy. The sequences can  
 CC also be used in the diagnosis and treatment of bacterial infections,  
 CC particularly S. epidermidis infections. The sequences can be used to  
 CC screen for compounds able to interfere with the S. epidermidis life cycle  
 CC or inhibit S. epidermidis infection. N.B. The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from the USPTO web site  
 XX Sequence 467 AA;  
 SQ Query Match 81.0%; Score 34; DB 5; Length 467;  
 Best Local Similarity 66.7%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 KNKEKALII 9  
 Db 27 KNKEKVLII 35  
 |||||  
 |||||  
 RESULT 13  
 ADM87702  
 ID ADM87702 standard; protein; 102 AA.  
 AC ADM87702;  
 XX 03-JUN-2004 (first entry)  
 DT Human EST derived amino acid sequence SEQ ID NO:795.  
 DE respiratory; cytostatic; antiarthritic; antiinflammatory;  
 XX gastrointestinal; antibacterial; immunosuppressive; antidiabetic;  
 KW antineoplastic; gene therapy; molecular weight marker; chromosome marker;  
 KW chromosome tag; genetic fingerprinting; nutritional supplement; cancer;  
 KW inflammatory condition; arthritis; inflammatory bowel disease;  
 KW Crohn's disease; sepsis; rheumatoid arthritis; diabetes mellitus type 1;  
 KW graft versus host disease; human; expressed sequence tag; EST.  
 OS Homo sapiens.  
 XX WO2004009834-A2.  
 XX 29-JAN-2004.  
 PD 19-JUL-2002; 2002WO-US022858.  
 PF 21-JUL-2001; 2001US-0306971P.  
 PR 28-MAR-2002; 2002US-00112944.  
 XX (NUVE-) NUVELO INC.  
 XX Tang YT, Yang Y, Wang G, Zhang J, Ren F, Xue A, Wang J;





OS Klebsiella pneumoniae.  
 XX US6610836-B1.  
 PN XX  
 XX 26-AUG-2003.  
 PD XX  
 XX 27-JAN-2000; 2000US-00489039.  
 PF XX  
 XX 29-JAN-1999; 99US-0117747P.  
 PR XX  
 XX (GENO-) GENOME THERAPEUTICS CORP.  
 PA XX  
 XX Breton GL, Osborne M;  
 PI XX  
 XX WPI; 2003-895346/82.  
 DR N-PSDB; ACH98546.  
 XX  
 PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for  
 PT preparing a vaccine composition against Klebsiella pneumoniae.  
 XX  
 PS Disclosure; SEQ ID NO 11512; 932pp; English.  
 XX  
 XX The invention describes a new isolated nucleic acid encoding a Klebsiella  
 CC pneumoniae polypeptide. Also described are: a recombinant expression  
 CC vector comprising the nucleic acid, operably linked to a transcription  
 CC regulatory element; and a cell comprising the recombinant expression  
 CC vector. The nucleic acid is useful for preparing a vaccine composition  
 CC against Klebsiella pneumoniae. This is the amino acid sequence of a  
 CC Klebsiella pneumoniae polypeptide of the invention  
 XX  
 SQ Sequence 181 AA;

Query Match 78.6%; Score 33; DB 7; Length 181;  
 Best Local Similarity 66.7%; Pred. No. 2e+02;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
 ||| |||:  
 Db 6 KNKAKALVL 14

Search completed: December 6, 2004, 15:26:09  
 Job time : 122 secs

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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:19:38 ; Search time 27.5 Seconds  
(without alignments)  
21.704 Million cell updates/sec

Title: US-10-042-202-17  
Perfect score: 42  
Sequence: 1 KNKEKALII 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Lasting first 45 summaries

Database : Issued Patents AA:\*  
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3: /cgn2\_6/ptodata/1/1aa/6A-COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B-COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	11	4	US-09-454-204A-8
2	42	100.0	229	4	US-09-454-204A-41
3	42	100.0	559	1	US-08-313-288B-14
4	35	83.3	227	3	US-09-134-001C-5420
5	34	81.0	198	4	US-09-248-796A-16240
6	34	81.0	224	4	US-09-252-991A-17505
7	34	81.0	299	4	US-09-270-767-35368
8	34	81.0	299	4	US-09-270-767-50585
9	34	81.0	467	3	US-09-134-001C-3452
10	33	78.6	181	4	US-09-489-039A-11512
11	32	76.2	166	4	US-09-107-532A-7230
12	32	76.2	269	3	US-08-652-877-5
13	32	76.2	269	3	US-08-476-515A-5
14	32	76.2	439	4	US-09-248-796A-18964
15	32	76.2	732	4	US-08-671-757A-7
16	32	76.2	732	4	US-08-671-757A-8
17	32	76.2	810	4	US-09-198-452A-20
18	32	76.2	810	4	US-09-198-452A-1128
19	32	76.2	884	6	5208144-8
20	31	73.8	116	4	US-09-134-000C-6570
21	31	73.8	300	4	US-09-861-451A-42
22	31	73.8	482	3	US-09-135-639-2
23	31	73.8	712	2	US-08-468-576B-17
24	31	73.8	712	2	US-08-468-579B-17
25	31	73.8	712	3	US-08-468-577B-17
26	31	73.8	777	4	US-09-543-681A-4272
27	30	71.4	60	4	US-09-248-796A-25586

28	71.4	97	4	US-09-107-532A-4024	Sequence 4024, Ap
29	71.4	142	4	US-09-583-110-3710	Sequence 3710, Ap
30	71.4	189	1	US-08-446-083-1	Sequence 1, Appli
31	71.4	189	4	US-09-248-796A-15896	Sequence 15896, A
32	71.4	201	4	US-09-543-681A-7854	Sequence 7854, Ap
33	71.4	215	4	US-09-107-532A-4220	Sequence 4220, Ap
34	71.4	231	4	US-09-248-796A-15210	Sequence 15210, A
35	71.4	249	4	US-09-198-452A-1131	Sequence 1131, Ap
36	71.4	295	4	US-09-248-796A-17527	Sequence 17527, A
37	71.4	306	2	US-08-736-723A-6	Sequence 6, Appli
38	71.4	306	3	US-09-221-114-6	Sequence 6, Appli
39	71.4	306	4	US-09-270-767-57870	Sequence 57870, A
40	71.4	337	4	US-09-780-996A-9	Sequence 9, Appli
41	71.4	359	3	US-09-155-920-2	Sequence 2, Appli
42	71.4	359	3	US-08-858-207A-389	Sequence 389, App
43	71.4	359	4	US-09-198-452A-131	Sequence 131, App
44	71.4	366	4	US-09-540-236-2711	Sequence 2711, Ap
45	71.4	371	4	US-09-270-767-42238	Sequence 42238, A

ALIGNMENTS

RESULT 1  
US-09-454-204A-8  
; Sequence 8, Application US/09454204A  
; Patent No. 6663871  
; GENERAL INFORMATION:  
; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg  
; APPLICANT: Plebanski, Magdalena  
; APPLICANT: Hanke, Tomas  
; APPLICANT: Smith, Geoffrey L.  
; APPLICANT: Blanchard, Tom  
; TITLE OF INVENTION: Methods and Reagents for Vaccination  
; FILE OF INVENTION: Which Generate A CD8 T Cell Immune Response  
; FILE REFERENCE: 2907.1000-000  
; CURRENT APPLICATION NUMBER: US/09/454,204A  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: PCT/GB98/01681  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: GB 97 11957.2  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: CTL Epitope of the Malaria String  
US-09-454-204A-8

Query Match 100.0%; Score 42; DB 4; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | | | | | | |  
DB 3 KNKEKALII 11

RESULT 2  
US-09-454-204A-41  
; Sequence 41, Application US/09454204A  
; Patent No. 6663871  
; GENERAL INFORMATION:  
; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg

```
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/09/454,204A
; CURRENT FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
; US-09-454-204A-41

Query Match      100.0%; Score 42; DB 4; Length 229;
Best Local Similarity 100.0%; Pred. No. 0.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNKEKALII 9
Db      58 KNKEKALII 66

RESULT 3
US-08-313-288B-14
; Sequence 14, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-SPONDIN
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/313,288B
; FILING DATE: January 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0526
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 559 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
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; ANTI-SENSE: NO
; US-08-313-288B-14

Query Match      100.0%; Score 42; DB 1; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNKEKALII 9
Db      109 KNKEKALII 117

RESULT 4
US-09-134-001C-5420
; Sequence 5420, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5420
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
; US-09-134-001C-5420

Query Match      83.3%; Score 35; DB 3; Length 227;
Best Local Similarity 75.0%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      2 NKEKALII 9
Db      11 NKEKALV 18

RESULT 5
US-09-248-796A-16240
; Sequence 16240, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 16240
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-16240

Query Match      81.0%; Score 34; DB 4; Length 198;
Best Local Similarity 77.8%; Pred. No. 29;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 KNKEKALII 9
Db      59 KNKEKSAII 67
```

## RESULT 6

US-09-252-991A-17505  
; Sequence 17505, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 17505  
; LENGTH: 224  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-17505

Query Match 81.0%; Score 34; DB 4; Length 224;  
Best Local Similarity 75.0%; Pred. No. 32;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 8

DB 129 KNKQKALV 136

## RESULT 7

US-09-270-767-35368  
; Sequence 35368, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 35368  
; LENGTH: 299  
; TYPE: PRT  
; ORGANISM: Drosophila melanogaster  
; FEATURE:  
; OTHER INFORMATION: Xaa means any amino acid  
US-09-270-767-35368

Query Match 81.0%; Score 34; DB 4; Length 299;  
Best Local Similarity 77.8%; Pred. No. 43;  
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9

DB 142 KNQEQALII 150

## RESULT 8

US-09-270-767-50585  
; Sequence 50585, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 50585

; LENGTH: 299

; TYPE: PRT

; ORGANISM: Drosophila melanogaster

; FEATURE:

; OTHER INFORMATION: Xaa means any amino acid

US-09-270-767-50585

Query Match 81.0%; Score 34; DB 4; Length 299;

Best Local Similarity 77.8%; Pred. No. 43;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9

DB 142 KNQEQALII 150

## RESULT 9

US-09-134-001C-3452  
; Sequence 3452, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 3452  
; LENGTH: 467  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-3452

Query Match 81.0%; Score 34; DB 3; Length 467;

Best Local Similarity 66.7%; Pred. No. 68;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNKEKALII 9

DB 27 KNKEKVLII 35

## RESULT 10

US-09-489-039A-11512  
; Sequence 11512, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 11512  
; LENGTH: 181  
; TYPE: PRT  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-11512

Query Match 78.6%; Score 33; DB 4; Length 181;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNKEKALII 9

```
Db      ||| |||::
        6 KNKAKALVL 14

RESULT 11
US-09-107-532A-7230
; Sequence 7230, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <unknown>
; SOFTWARE: ASCII
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107.532A
; FILING DATE: 30-Jun-1998
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-8277
; TELEFAX: (781)893-8277
;
; INFORMATION FOR SEQ ID NO: 7230:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...166
; SEQUENCE DESCRIPTION: SEQ ID NO: 7230:
US-09-107-532A-7230

Query Match 76.2%; Score 32; DB 4; Length 166;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KNKEKALII 9
Db      33 KNKEAFLLI 41

RESULT 12
US-08-652-877-5
; Sequence 5, Application US/08652877
; Patent No. 6187548
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
;
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky

APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
APPLICANT: Hjalms, Goran
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcoia Rd., 3C43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355B-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-652-877-5

Query Match 76.2%; Score 32; DB 3; Length 269;
Best Local Similarity 55.6%; Pred. No. 96;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KNKEKALII 9
Db      166 ENKERVLIV 174

RESULT 13
US-08-476-515A-5
; Sequence 5, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Akerstrom, Goran
; APPLICANT: Juhlin, Claes
; APPLICANT: Rask, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjalms, Goran
;
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
```



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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:18:43 ; Search time 23.5 Seconds  
(without alignments)  
36.849 Million cell updates/sec

Title: US-10-042-202-17  
Perfect score: 42  
Sequence: 1 KNKEKALII 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	559	2 S04531	thrombospondin-rel
2	42	100.0	574	2 A46283	sporozoite surface
3	38	90.5	177	2 AD1251	modulates DNA topo
4	38	90.5	177	2 S70846	flar protein - Lis
5	37	88.1	497	2 A84956	UDP-N-acetylmuram
6	36	85.7	468	2 F70406	conserved hypothet
7	35	83.3	174	2 D84676	hypothetical prote
8	35	83.3	222	2 C97345	PP-loop superfamil
9	35	83.3	4919	2 T31105	hypothetical prote
10	34	81.0	216	2 S37351	algf protein precu
11	34	81.0	216	2 A83201	arginate o-acetyl
12	34	81.0	350	2 D84994	A/G-specific adeni
13	33	78.6	154	2 S55630	hypothetical prote
14	33	78.6	320	2 F9570	unknown protein, 8
15	33	78.6	372	1 S76448	translation releas
16	33	78.6	443	2 B99952	conserved hypothet
17	33	78.6	465	2 D84636	hypothetical prote
18	33	78.6	518	2 AD1731	hypothetical prote
19	33	78.6	698	2 AD2237	ATP-dependent DNA
20	33	78.6	1005	2 A64465	hypothetical prote
21	32	76.2	164	2 T47547	hypothetical prote
22	32	76.2	232	2 T43754	hypothetical prote
23	32	76.2	241	2 H81536	hypothetical prote
24	32	76.2	352	2 E64529	translation releas
25	32	76.2	352	2 F71977	translation releas
26	32	76.2	356	1 S55437	peptide chain rele
27	32	76.2	356	2 G84121	protein chain rele
28	32	76.2	359	2 H97254	frame-shift with c
29	32	76.2	456	2 B72130	

30	32	76.2	561	2 T45607	hypothetical prote
31	32	76.2	733	2 A64650	flagellar biosynth
32	32	76.2	733	2 E71937	flagellar biosynth
33	32	76.2	774	2 B86492	hypothetical prote
34	32	76.2	774	2 H81540	hypothetical prote
35	32	76.2	811	2 E72003	hypothetical prote
36	32	76.2	972	2 A30363	glycoprotein GP330
37	32	76.2	1650	2 S53457	dominant autoantig
38	32	76.2	4572	2 S57908	hypothetical 527K
39	32	76.2	4660	2 T42737	gp330 protein prec
40	31	73.8	114	2 B51117	hypothetical prote
41	31	73.8	126	2 JQ1539	hypothetical 14.5K
42	31	73.8	227	2 F97276	CPS3/CAPA conserve
43	31	73.8	227	2 E97274	CPS3/CAPA conserve
44	31	73.8	229	2 AD1021	probable exported
45	31	73.8	229	2 D91261	hypothetical prote

ALIGNMENTS

RESULT 1

S04531

thrombospondin-related protein TRAP - malaria parasite (Plasmodium falciparum)  
N:Alternate names: thrombospondin-related anonymous protein  
C:Species: Plasmodium falciparum  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004  
C:Accession: S04531

R:Robson, K.J.H.; Hall, J.R.S.; Jennings, M.W.; Harris, T.J.R.; Marsh, K.; Newbold, C.I.;

Nature 335, 79-82, 1988

A:Title: A highly conserved amino-acid sequence in thrombospondin, properdin and in prote

A:Reference number: S04531; MUID:88318952; PMID:3045563

A:Accession: S04531

A:Molecule type: DNA

A:Residues: 1-559 <ROB>

A:Cross-references: UNIPROT:P16893; EMBL:X13022; NID:g9977; PID:g9978

F:240-287/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 100.0%; Score 42; DB 2; Length 559;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
DB 109 KNKEKALII 117

RESULT 2

A46283

sporozoite surface protein 2 - malaria parasite (Plasmodium falciparum) (strain NFS4)  
N:Alternate names: thrombospondin-related anonymous protein (TRAP)  
C:Species: Plasmodium falciparum

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004

C:Accession: A46283

R:Rogers, W.O.; Malik, A.; Mellouk, S.; Nakamura, K.; Rogers, M.D.; Szarfman, A.; Gordon,

Proc. Natl. Acad. Sci. U.S.A. 89, 9176-9180, 1992

A:Title: Characterization of Plasmodium falciparum sporozoite surface protein 2.

A:Reference number: A46283; MUID:93028427; PMID:1409621

A:Accession: A46283

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-574 <ROG>

A:Cross-references: UNIPROT:Q26020; GB:M94013; NID:g160690; PID:g160691

F:240-287/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 100.0%; Score 42; DB 2; Length 574;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
DB 109 KNKEKALII 117

```
RESULT 3
AD1251
modulates DNA topology [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1251
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
Science 294, 849-852, 2001
A;Authors: Krefte, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maqueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AD1251
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <GLA>
A;Cross-references: UNIPROT:Q48753; GB:NC_003210; PIDN:CAC99490.1; PID:g16410841; GSPDB:
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1412

Query Match 90.5%; Score 38; DB 2; Length 177;
Best Local Similarity 88.9%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
| | | | |
DB 12 KNKEKVLII 20

RESULT 4
S70846
flar protein - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S70846
R;Sanchez-Campillo, M.; Dramsi, S.; Gomez-Gomez, J.M.; Michel, E.; Deboux, P.; Cossart,
Mol. Microbiol. 18, 801-811, 1995
A;Title: Modulation of DNA topology by flar, a new gene, from Listeria monocytogenes.
A;Reference number: S70846; MUID:56422467; PMID:8825084
A;Accession: S70846
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-177 <SAN>
A;Cross-references: UNIPROT:Q48753; EMBL:U29951; NID:g1036787; PIDN:AAB50026.1; PID:g103
A;Genetics:
A;Gene: flar

Query Match 90.5%; Score 38; DB 2; Length 177;
Best Local Similarity 88.9%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
| | | | |
DB 12 KNKEKVLII 20

RESULT 5
A84956
UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diamino-pimelate ligase (EC 6.3.2.13) [import
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 03-Jun-2002
C;Accession: A84956
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A;Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A;Reference number: A84956; MUID:20445173; PMID:10993077
A;Accession: A84956
A;Status: preliminary
A;Molecule type: DNA
```

```
A;Residues: 1-497 <STO>
A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
C;Genetics:
A;Gene: murE; BU221
C;Superfamily: UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase
C;Keywords: ligase

Query Match 88.1%; Score 37; DB 2; Length 497;
Best Local Similarity 88.9%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
| | | | |
DB 435 KNKEKILII 443

RESULT 6
F70406
conserved hypothetical protein aq_1236 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: F70406
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ove
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: F70406
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-468 <AQF>
A;Cross-references: UNIPROT:O67281; GB:AE000730; NID:g2983674; PIDN:AAC07253.1; PID:g298;
A;Experimental source: strain VFS
C;Genetics:
A;Gene: aq_1236

Query Match 85.7%; Score 36; DB 2; Length 468;
Best Local Similarity 87.5%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 8
| | | | |
DB 102 KNKEKALI 109

RESULT 7
D84676
hypothetical protein At2g27740 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cross)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: D84676
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
eues, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: D84676
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-174 <STO>
A;Cross-references: UNIPROT:Q9ZUX5; GB:AE002093; NID:g3860258; PIDN:AAC73026.1; GSPDB:GN
C;Genetics:
A;Gene: At2g27740
A;Map position: 2

Query Match 83.3%; Score 35; DB 2; Length 174;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
| | | | |
```

Db 136 KNKEKAIFV 144

RESULT 8  
C97345  
PP-loop superfamily ATPase, confers aluminum resistance [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C:Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 09-Jul-2004  
C:Accession: C97345  
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: C97345  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-222 <KUR>  
A:Cross-references: UNIPROT:Q97D53; GB:AE001437; PIDN:AAK81550.1; PID:gl5026727; GSPDB:G000000000  
A:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3627  
C:Superfamily: conserved hypothetical protein H1191

Query Match 83.3%; Score 35; DB 2; Length 222;  
Best Local Similarity 75.0%; Pred. No. 14;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 NKEKALII 9  
|||||:  
6 NKEKALVV 13

RESULT 9  
T31105  
Hypothetical protein 2 - Haemophilus ducreyi  
C:Species: Haemophilus ducreyi  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C:Accession: T31105  
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.  
J. Bacteriol. 180, 6013-6022, 1998  
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.  
A:Reference number: Z20984; MUID:99030326; PMID:9811662  
A:Accession: T31105  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-4919 <WAR>  
A:Cross-references: UNIPROT:Q9ZHL0; EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AACT31105  
C:Genetics:  
A:Gene: lrpA2

Query Match 83.3%; Score 35; DB 2; Length 4919;  
Best Local Similarity 87.5%; Pred. No. 2.8e+02;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 NKEKALII 9  
|||||:  
700 NKEKALIL 707

RESULT 10  
S37351  
algF protein precursor - Pseudomonas aeruginosa  
C:Species: Pseudomonas aeruginosa  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 09-Jul-2004  
C:Accession: S37351; S38858  
R:Shinabarger, D.; May, T.B.; Boyd, A.; Ghosh, M.; Chakraborty, A.M.  
Mol. Microbiol. 9, 1027-1035, 1993  
A:Title: Nucleotide sequence and expression of the Pseudomonas aeruginosa algF gene controlled by the algB promoter  
A:Reference number: S37351; MUID:95020624; PMID:7934909  
A:Accession: S37351  
A:Molecule type: DNA  
A:Residues: 1-216 <SH11>

A:Cross-references: UNIPROT:Q06062; EMBL:LI3026; NID:g294339; PIDN:AAD15231.1; PID:g294343  
A:Accession: S38858  
A:Molecule type: protein  
A:Residues: 29-39 <SH12>  
C:Genetics:  
A:Gene: algF  
C:Superfamily: Pseudomonas aeruginosa algF protein  
F:1-26/Domain: signal sequence #status predicted <SIG>  
F:29-216/Product: algF protein #status experimental <MAT>

Query Match 81.0%; Score 34; DB 2; Length 216;  
Best Local Similarity 75.0%; Pred. No. 21;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 8  
|||||:  
121 KNKQKALV 128

Db 121 KNKQKALV 128

RESULT 11  
A83201  
alginatase o-acetyltransferase AlgF PA3550 [imported] - Pseudomonas aeruginosa (strain PAO1)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: A83201  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Briadman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen  
A:Reference number: A82950; MUID:20437337; PMID:10984043  
A:Accession: A83201  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-216 <STO>  
A:Cross-references: UNIPROT:Q06062; GB:AE004776; GB:AE004091; NID:g9949701; PIDN:AAG06938  
A:Experimental source: strain PAO1  
C:Genetics:  
A:Gene: algF; PA3550  
C:Superfamily: Pseudomonas aeruginosa algF protein

Query Match 81.0%; Score 34; DB 2; Length 216;  
Best Local Similarity 75.0%; Pred. No. 21;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 8  
|||||:  
121 KNKQKALV 128

Db 121 KNKQKALV 128

RESULT 12  
D84994  
A/G-specific adenine glycosylase [imported] - Buchnera sp. (strain APS)  
C:Species: Buchnera sp.  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 23-Mar-2001  
C:Accession: D84994  
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.  
Nature 407, 81-86, 2000  
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. At  
A:Reference number: A84930; MUID:20445173; PMID:10993077  
A:Accession: D84994  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-350 <STO>  
A:Cross-references: GB:AP000398; GSPDB:GN00144  
A:Experimental source: strain APS  
C:Genetics:  
A:Gene: mutY; BU552  
C:Superfamily: A/G-specific adenine glycosylase

Query Match 81.0%; Score 34; DB 2; Length 350;  
Best Local Similarity 87.5%; Pred. No. 34;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 8  
|||||  
Db 265 KNKEKALI 272

RESULT 13

S55630  
hypothetical protein 35 - equine herpesvirus 2  
C:Species: equine herpesvirus 2  
C:Date: 27-Oct-1995 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S55630  
R:Telford, E.A.R.; Watson, M.S.; Aird, H.C.; Perry, J.; Davison, A.J.  
J. Mol. Biol. 249, 520-528, 1995  
A:Title: The DNA sequence of equine herpesvirus 2.  
A:Reference number: S55594; MUID:95302501; PMID:7783207  
A:Accession: S55630  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-154 <TEL>  
A:Cross-references: UNIPROT:Q66639; GB:U20824; NID:G695172; PIDN:AAAC13823.1; PID:G695208  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1995

Query Match 78.6%; Score 33; DB 2; Length 154;  
Best Local Similarity 75.0%; Pred. No. 24;  
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 8  
|||||  
Db 77 KNKEKALI 84

RESULT 14

F96570  
unknown protein, 80333-82175 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: F96570  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizlar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: F96570  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-320 <STO>  
A:Cross-references: UNIPROT:Q9C928; GB:AE005173; NID:G6862953; PIDN:AAF30341.1; GSPDB:GN  
C:Genetics:  
A:Gene: F14G24.20  
A:Map position: 1  
C:Superfamily: probable membrane protein YOLO77c

Query Match 78.6%; Score 33; DB 2; Length 320;  
Best Local Similarity 75.0%; Pred. No. 49;  
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 8  
|||||  
Db 54 KNKEKALI 61

RESULT 15

S76448  
translation releasing factor RF-2 - Synchocystis sp. (strain PCC 6803)  
N:Alternate names: peptide chain release factor 2  
C:Species: Synchocystis sp.

A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 06-Jun-1997 #text\_change 09-Jul-2004  
C:Accession: S76448  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;  
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis  
S.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S76448  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-372 <KAN>  
A:Cross-references: UNIPROT:P74476; EMBL:D90915; GB:AB001339; NID:G1653604  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Comment: This is one of two codon-specific peptide-chain-release factors that are resp  
ion codons UGA and UAA.  
C:Comment: The gene coding for this protein (RF-2) contains a UGA in-frame termination co  
action of RF-2. This provides a mechanism for the protein to regulate its own production.  
C:Genetics:  
A:Gene: prfB  
C:Superfamily: translation releasing factor  
C:Keywords: protein biosynthesis; translational frameshift  
F;26-27/Region: plus-one translational frameshift

Query Match 78.6%; Score 33; DB 1; Length 372;  
Best Local Similarity 77.8%; Pred. No. 57;  
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALI 9  
|||||  
Db 284 KNKEKALI 292

Search completed: December 6, 2004, 15:31:10  
Job time : 24.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:17:52 ; Search time 125.5 Seconds  
(without alignments)  
41.262 Million cell updates/sec

Title: US-10-042-202-17  
Perfect score: 42  
Sequence: 1 KNKERALII 9

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	327	2 Q70GJ7	Q70GJ7 plasmodium
2	42	100.0	327	2 CAE46498	CAE46498 plasmodiu
3	42	100.0	331	2 Q70GE3	Q70GE3 plasmodium
4	42	100.0	331	2 Q70GJ8	Q70GJ8 plasmodium
5	42	100.0	331	2 Q70GK2	Q70GK2 plasmodium
6	42	100.0	331	2 Q70GK3	Q70GK3 plasmodium
7	42	100.0	331	2 CAE46492	CAE46492 plasmodiu
8	42	100.0	331	2 CAE46493	CAE46493 plasmodiu
9	42	100.0	331	2 CAE46497	CAE46497 plasmodiu
10	42	100.0	331	2 CAE46626	CAE46626 plasmodiu
11	42	100.0	559	1 TRAP PLAF4	TRAP PLAF4
12	42	100.0	559	2 Q76109	Q76109 plasmodium
13	42	100.0	559	2 Q76111	Q76111 plasmodium
14	42	100.0	559	2 Q76112	Q76112 plasmodium
15	42	100.0	559	2 Q76113	Q76113 plasmodium
16	42	100.0	559	2 Q76114	Q76114 plasmodium
17	42	100.0	559	2 Q76117	Q76117 plasmodium
18	42	100.0	559	2 Q76118	Q76118 plasmodium
19	42	100.0	559	2 Q01502	Q01502 plasmodium
20	42	100.0	559	2 Q01503	Q01503 plasmodium
21	42	100.0	559	2 Q01506	Q01506 plasmodium
22	42	100.0	559	2 Q01508	Q01508 plasmodium
23	42	100.0	559	2 Q01509	Q01509 plasmodium
24	42	100.0	559	2 Q717T6	Q717T6 plasmodium
25	42	100.0	559	2 Q717T7	Q717T7 plasmodium
26	42	100.0	559	2 Q717T9	Q717T9 plasmodium
27	42	100.0	559	2 Q717U0	Q717U0 plasmodium
28	42	100.0	559	2 Q9TYC1	Q9TYC1 plasmodium
29	42	100.0	559	2 Q9TYC2	Q9TYC2 plasmodium
30	42	100.0	559	2 Q9TYC3	Q9TYC3 plasmodium
31	42	100.0	559	2 Q9TYC4	Q9TYC4 plasmodium

32 42 100.0 559 2 Q9TYC5 Q9TYC5 plasmodium  
33 42 100.0 559 2 Q9TYC6 Q9TYC6 plasmodium  
34 42 100.0 559 2 Q9TYC7 Q9TYC7 plasmodium  
35 42 100.0 559 2 Q9TYC8 Q9TYC8 plasmodium  
36 42 100.0 559 2 Q9TYD0 Q9TYD0 plasmodium  
37 42 100.0 559 2 Q9TYD1 Q9TYD1 plasmodium  
38 42 100.0 559 2 Q9TYD2 Q9TYD2 plasmodium  
39 42 100.0 559 2 Q9GTW7 Q9GTW7 plasmodium  
40 42 100.0 559 2 AAQ11891 AAQ11891 plasmodiu  
41 42 100.0 559 2 AAQ11892 AAQ11892 plasmodiu  
42 42 100.0 559 2 AAQ11893 AAQ11893 plasmodiu  
43 42 100.0 559 2 AAQ11894 AAQ11894 plasmodiu  
44 42 100.0 559 2 AAQ11895 AAQ11895 plasmodiu  
45 42 100.0 562 2 Q01510 Q01510 plasmodium

ALIGNMENTS

RESULT 1  
Q70GJ7 PRELIMINARY; PRT; 327 AA.  
AC Q70GJ7;  
DT 05-JUL-2004 (TREMBLrel. 27, Created)  
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
DE Trap protein (Fragment).  
GN Name:trap;  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Mamillapalli A., Joshi H., Malhotra P.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ581771; CAE46498.1; -  
DR InterPro; IPR000884; TSP1.  
DR InterPro; IPR002035; VWF A.  
DR Pfam; PF00090; TSP 1; 1.  
DR Pfam; PF00092; VWA\_1; 1.  
DR PRINTS; PRO0453; VWFADOMAIN.  
DR SMART; SM00209; TSP1; 1.  
DR SMART; SM00327; VWA; 1.  
DR PROSITE; PS00092; TSP1; 1.  
DR PROSITE; PS0234; VWEA; 1.  
FT NON\_TER 327  
SQ SEQUENCE 327 AA; 37251 MW; 881D7A4B4EDD235A CRC64;

Query Match 100.0%; Score 42; DB 2; Length 327;  
Best Local Similarity 100.0%; Pred. NO. 4.9;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKERALII 9  
DB 105 KNKERALII 113

RESULT 2  
CAE46498 PRELIMINARY; PRT; 327 AA.  
ID CAE46498;  
AC CAE46498;  
DT 02-MAR-2004 (TREMBLrel. 27, Created)  
DT 02-MAR-2004 (TREMBLrel. 27, Last sequence update)  
DE Trap protein (Fragment).  
GN TRAP..  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DK3-16;  
RA Mamillapalli A., Joshi H., Malhotra P.;

```
RT "Polymorphism in TRAP N-terminal region of Plasmodium falciparum in
RT Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581771; CAE46498.1; -.
FT NON TER 327
SQ SEQUENCE 327 AA; 37251 MW; 881D7A4B4EDD235A CRC64;

Query Match 100.0%; Score 42; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNKEKALII 9
Db 105 KNKEKALII 113

RESULT 3
Q70GE3 Q70GE3 PRELIMINARY; PRT; 331 AA.
AC Q70GE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trombospondin-related protein (Fragment).
DE Name-trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ582081; CAE46626.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP.1; 1.
DR Pfam; PF00092; VWA.1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSP1.1.
DR SMART; SM00327; VWA.1.
DR PROSITE; PS50092; TSP1.1.
DR PROSITE; PS50234; VWF_A.1.
FT NON TER 331
SQ SEQUENCE 331 AA; 37559 MW; BIBFCC83B8BD4D25 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNKEKALII 9
Db 109 KNKEKALII 117

RESULT 4
Q70GJ8 Q70GJ8 PRELIMINARY; PRT; 331 AA.
AC Q70GJ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trap protein (Fragment).
DE Name-trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581770; CAE46497.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.

RT "Polymorphism in TRAP N-terminal region of Plasmodium falciparum in
RT Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581771; CAE46498.1; -.
FT NON TER 327
SQ SEQUENCE 327 AA; 37251 MW; 881D7A4B4EDD235A CRC64;

Query Match 100.0%; Score 42; DB 2; Length 327;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNKEKALII 9
Db 105 KNKEKALII 113

RESULT 3
Q70GE3 Q70GE3 PRELIMINARY; PRT; 331 AA.
AC Q70GE3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trombospondin-related protein (Fragment).
DE Name-trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ582081; CAE46626.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP.1; 1.
DR Pfam; PF00092; VWA.1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSP1.1.
DR SMART; SM00327; VWA.1.
DR PROSITE; PS50092; TSP1.1.
DR PROSITE; PS50234; VWF_A.1.
FT NON TER 331
SQ SEQUENCE 331 AA; 37559 MW; BIBFCC83B8BD4D25 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNKEKALII 9
Db 109 KNKEKALII 117

RESULT 4
Q70GJ8 Q70GJ8 PRELIMINARY; PRT; 331 AA.
AC Q70GJ8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trap protein (Fragment).
DE Name-trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581770; CAE46497.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.

DR Pfam; PF00090; TSP.1; 1.
DR Pfam; PF00092; VWA.1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSP1.1.
DR SMART; SM00327; VWA.1.
DR PROSITE; PS50092; TSP1.1.
DR PROSITE; PS50234; VWF_A.1.
FT NON TER 331
SQ SEQUENCE 331 AA; 37559 MW; 2FE4EB47F1963D76 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KNKEKALII 9
Db 109 KNKEKALII 117

RESULT 6
Q70GK3 Q70GK3 PRELIMINARY; PRT; 331 AA.
AC Q70GK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Trap protein (Fragment).
DE Name-trap;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Mamillapalli A., Joshi H., Malhotra P.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AJ581764; CAE46492.1; -.
DR InterPro; IPR000884; TSPI.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00092; VWA_1; 1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSPI.1.
DR SMART; SM00327; VWA; 1.
DR PROSITE; PS00092; TSPI.1.
DR PROSITE; PS0234; VWA; 1.
FT NON_TER 331
SQ SEQUENCE 331 AA; 37625 MW; 4258443729D48835 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
Db 109 KNKEKALII 117

RESULT 7
CAE46492
ID CAE46492 PRELIMINARY; PRT; 331 AA.
AC CAE46492;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Trap protein (Fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM3-51;
RA Mamillapalli A., Joshi H., Malhotra P.;
RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581764; CAE46492.1; -.
FT NON_TER 331
SQ SEQUENCE 331 AA; 37625 MW; 4258443729D48835 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
Db 109 KNKEKALII 117

RESULT 8
CAE46493
ID CAE46493 PRELIMINARY; PRT; 331 AA.
AC CAE46493;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Trap protein (Fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM3-21;
RA Mamillapalli A., Joshi H., Malhotra P.;
RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ581765; CAE46493.1; -.
FT NON_TER 331
SQ SEQUENCE 331 AA; 37609 MW; 2PB4EB47F1963D76 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
Db 109 KNKEKALII 117

RESULT 9
CAE46497
ID CAE46497 PRELIMINARY; PRT; 331 AA.
AC CAE46497;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Trap protein (Fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CM3-56;
RA Mamillapalli A., Joshi H., Malhotra P.;
RT "Polymorphism in TRAP-N terminal region of Plasmodium falciparum in Indian isolates.";
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ581770; CAE46497.1; -.
FT NON_TER 331
SQ SEQUENCE 331 AA; 37521 MW; CBD1823A0C8C49EB CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
Db 109 KNKEKALII 117

RESULT 10
CAE46626
ID CAE46626 PRELIMINARY; PRT; 331 AA.
AC CAE46626;
DT 02-MAR-2004 (TREMBlrel. 27, Created)
DT 02-MAR-2004 (TREMBlrel. 27, Last sequence update)
DE Trombospondin-related protein (fragment).
GN TRAP.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PP3-12;
RA Mamillapalli A., Joshi H., Malhotra P.;
RT "Polymorphism in TRAP N-terminal region of Plasmodium falciparum in Indian isolates.";
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ582081; CAE46626.1; -.
FT NON_TER 331
SQ SEQUENCE 331 AA; 37559 MW; B1BFCC83B8BD4D25 CRC64;

Query Match 100.0%; Score 42; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9
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Db 109 KNKEKALII 117
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TRAP_PLAFA STANDARD; PRT; 559 AA.
AC P16893;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Thrombospondin related anonymous protein precursor.
GN Name=TRAP;
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98319420; PubMed=3045563;
RA Jongtuites S., Putaporntip C., Kanbara H., Tanabe K.,
RA Robson K.J.H., Hall J.R.S., Jennings M.W., Harris T.J.R., Marsh K.,
RA Newbold C.I., Tate V.E., Weatherall D.J.;
RT "A highly conserved amino-acid sequence in thrombospondin, properdin
RT and in proteins from sporozoites and blood stages of a human malaria
RT parasite.";
RL Nature 335:79-82(1988).
CC -!- DEVELOPMENTAL STAGE: Expressed during erythrocytic stage of life
CC cycle.
CC -!- SIMILARITY: Contains 1 TSP type-1 domain.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X13022; CAA31440.1; -.
DR F1R; S04531; S04531.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00092; VWF_1.
DR PRINTS; PR00453; VWFADOMAIN.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00327; VWF; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Antigen; Cell adhesion; Glycoprotein; Malaria; Signal; Transmembrane.
FT SIGNAL 1
FT CHAIN 26 559
FT DOMAIN 48 234
FT DOMAIN 241 287
FT SITE 307 309
FT CROSSLNK 77 77
FT CROSSLNK 78 78
FT CROSSLNK 78 78
FT CARBOHYD 132 132
FT CARBOHYD 310 310
FT CARBOHYD 460 460
FT CARBOHYD 468 468
SQ SEQUENCE 559 AA; 63300 MW; 02A20164D198C37A CRC64;
Query Match 100.0%; Score 42; DB 1; Length 559;
Best Local Similarity 100.0%; Pred. No. 8.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

Db 109 KNKEKALII 117
|||||
PRELIMINARY; PRT; 559 AA.
AC 076109;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Thrombospondin-related protein (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98319420; PubMed=9657338;
RA Jongtuites S., Putaporntip C., Kanbara H., Tanabe K.;
RT "Variation in the thrombospondin-related adhesive protein (TRAP) gene
RT of Plasmodium falciparum from Thai field isolates.";
RL Mol. Biochem. Parasitol. 92:349-353(1998).
DR EMBL; AB006331; BAA31167.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00092; VWF_1.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00327; VWF; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER 559 559
SQ SEQUENCE 559 AA; 63409 MW; 9FAD7D0842DDB3EF CRC64;
Query Match 100.0%; Score 42; DB 2; Length 559;
Best Local Similarity 100.0%; Pred. No. 8.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 KNKEKALII 9
|||||
Db 109 KNKEKALII 117
|||||
PRELIMINARY; PRT; 559 AA.
AC 076111;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Thrombospondin-related protein (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98319420; PubMed=9657338;
RA Jongtuites S., Putaporntip C., Kanbara H., Tanabe K.;
RT "Variation in the thrombospondin-related adhesive protein (TRAP) gene
RT of Plasmodium falciparum from Thai field isolates.";
RL Mol. Biochem. Parasitol. 92:349-353(1998).
DR EMBL; AB006334; BAA31170.1; -.
DR InterPro; IPR000884; TSP1.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF00090; TSP_1; 1.
DR Pfam; PF00092; VWF_1.
DR SMART; SM00209; TSP1; 1.
DR SMART; SM00327; VWF; 1.
DR PROSITE; PS50092; TSP1; 1.
DR PROSITE; PS50234; VWFA; 1.
FT NON_TER 559 559
SQ SEQUENCE 559 AA; 63304 MW; DA2AC97D8EB1324 CRC64;
Query Match 100.0%; Score 42; DB 2; Length 559;
Best Local Similarity 100.0%; Pred. No. 8.4; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 KNKEKALII 9
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 15:26:21 ; Search time 99 Seconds  
(without alignments)  
32.420 Million cell updates/sec

Title: US-10-042-202-17

Perfect score: 42

Sequence: 1 KMKERALLI 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	100.0	9	13	US-10-042-202-17
2	42	100.0	9	14	US-10-360-836-19
3	42	100.0	11	14	US-10-079-167-8
4	42	100.0	11	16	US-10-653-624-8
5	42	100.0	11	16	US-10-833-439-8
6	42	100.0	11	17	US-10-833-745-8
7	42	100.0	11	17	US-10-833-744-8
8	42	100.0	11	17	US-10-686-943-8
9	42	100.0	229	14	US-10-079-167-41
10	42	100.0	229	16	US-10-653-624-41
11	42	100.0	229	16	US-10-833-439-41
12	42	100.0	229	17	US-10-833-745-41
13	42	100.0	229	17	US-10-833-744-41

14	100.0	229	17	US-10-686-943-41	Sequence 41, Appl
15	92.9	119	16	US-10-437-963-105530	Sequence 105530,
16	92.9	398	16	US-10-437-963-105528	Sequence 105528,
17	81.0	9	13	US-10-042-202-16	Sequence 16, Appl
18	81.0	9	14	US-10-360-836-18	Sequence 18, Appl
19	81.0	169	16	US-10-767-701-51339	Sequence 51339, A
20	81.0	170	17	US-10-425-115-258789	Sequence 258789,
21	81.0	176	15	US-10-425-114-57534	Sequence 57534, A
22	81.0	200	15	US-10-425-114-55246	Sequence 55246, A
23	81.0	637	17	US-10-425-115-193760	Sequence 193760,
24	78.6	72	15	US-10-424-599-191816	Sequence 191816,
25	78.6	102	15	US-10-112-944-795	Sequence 795, App
26	78.6	173	15	US-10-424-599-207348	Sequence 207348,
27	78.6	306	14	US-10-369-493-16611	Sequence 16611, A
28	78.6	369	15	US-10-112-944-340	Sequence 340, App
29	78.6	440	17	US-10-739-930-6741	Sequence 6741, Ap
30	76.2	1005	14	US-10-369-493-1061	Sequence 1061, Ap
31	76.2	137	15	US-10-282-122A-68338	Sequence 68338, A
32	76.2	173	15	US-10-424-599-228418	Sequence 228418,
33	76.2	233	15	US-10-335-977-4775	Sequence 4775, Ap
34	76.2	234	15	US-10-335-977-4774	Sequence 4774, Ap
35	76.2	259	17	US-10-335-977-4776	Sequence 4776, Ap
36	76.2	342	15	US-10-425-115-283479	Sequence 283479,
37	76.2	342	15	US-10-335-977-11287	Sequence 11287, A
38	76.2	352	9	US-09-815-242-11287	Sequence 11287, A
39	76.2	352	15	US-10-282-122A-58614	Sequence 58614, A
40	76.2	352	15	US-10-335-977-7167	Sequence 7167, Ap
41	76.2	354	15	US-10-335-977-7168	Sequence 7168, Ap
42	76.2	355	15	US-10-282-122A-45406	Sequence 45406, A
43	76.2	358	15	US-10-282-122A-52257	Sequence 52257, A
44	76.2	359	15	US-10-282-122A-51760	Sequence 51760, A
45	76.2	391	15	US-10-424-599-198244	Sequence 198244,

#### ALIGNMENTS

#### RESULT 1

US-10-042-202-17  
; Sequence 17, Application US/10042202  
; Publication NO. US20020136733A1

GENERAL INFORMATION:  
APPLICANT: Adrian Vivian Sinton HILL, Michael AIDOO,

Catherine Elizabeth Margaret Alisopp, Ajit LALVANI, Magdalena

PIEBANSKI, Hilton Carter WHITTLE,

TITLE OF INVENTION: MALARIA PEPTIDES

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:

ADDRESSEE: WENDERTH, LIND & PONACK, L.L.P.

STREET: 2033 K Street,N.W., Suite 800,

CITY: Washington

STATE: D.C.,

COUNTRY: U.S.A.

ZIP: 20006-1021

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPad for Windows 95

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/042,202

FILING DATE: 11-Jan-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/714,175

FILING DATE: 28-JAN-1997

APPLICATION NUMBER: WO PCT/GB95/26982

FILING DATE: 30-MAR-1995

APPLICATION NUMBER: GB 9406492.0

FILING DATE: 31-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Warren M Cheek, Jr.

REGISTRATION NUMBER: 33,367

REFERENCE/DOCKET NUMBER: 2002\_0026

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)-721-8200  
; TELEFAX: (202)-721-8250  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 9 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: <Unknown>  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-10-042-202-17

Query Match 100.0%; Score 42; DB 13; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
Db 1 KNKEKALII 9

## RESULT 2

US-10-360-836-19  
; Sequence 19, Application US/10360836  
; Publication No. US2003018584A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavala, Fidel  
; TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE  
; TITLE OF INVENTION: PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS  
; TITLE OF INVENTION: AND MALIGNANCIES  
; FILE REFERENCE: 5986/1J876  
; CURRENT APPLICATION NUMBER: US/10/360,836  
; CURRENT FILING DATE: 2003-02-07  
; PRIOR FILING DATE: 2003-02-07  
; PRIOR FILING DATE: 2002-02-08  
; NUMBER OF SEQ ID NOS: 86  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Plasmodium  
US-10-360-836-19

Query Match 100.0%; Score 42; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
Db 1 KNKEKALII 9

## RESULT 3

US-10-079-167-8  
; Sequence 8, Application US/10079167  
; Publication No. US20030138454A1  
; GENERAL INFORMATION:  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: McShane, Helen  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Reece, William  
; APPLICANT: Schneider, Joerg  
; TITLE OF INVENTION: Vaccination Method  
; FILE REFERENCE: 2907.1000-001  
; CURRENT APPLICATION NUMBER: US/10/079,167  
; CURRENT FILING DATE: 2002-02-19  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: PCT/GB98/01681  
; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: GB 97 11957.2  
; PRIOR FILING DATE: 1997-06-09  
; PRIOR APPLICATION NUMBER: PCT/GB01/04116  
; PRIOR FILING DATE: 2001-09-13  
; PRIOR APPLICATION NUMBER: GB 00 23203.3  
; PRIOR FILING DATE: 2001-09-21  
; NUMBER OF SEQ ID NOS: 99  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: CTL Epitope of the Malaria String  
US-10-079-167-8

Query Match 100.0%; Score 42; DB 14; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
Db 3 KNKEKALII 11

## RESULT 4

US-10-653-624-8  
; Sequence 8, Application US/10653624  
; Publication No. US20040131594A1  
; GENERAL INFORMATION:  
; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Joerg  
; APPLICANT: Piebanski, Magdalena  
; APPLICANT: Hanke, Tomas  
; APPLICANT: Smith, Geoffrey L.  
; APPLICANT: Blanchard, Tom  
; TITLE OF INVENTION: Methods and Reagents for Vaccination  
; TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response  
; FILE REFERENCE: 2907.1000-000  
; CURRENT APPLICATION NUMBER: US/10/653,624  
; CURRENT FILING DATE: 2003-09-02  
; PRIOR APPLICATION NUMBER: US/09/454,204A  
; PRIOR FILING DATE: 1999-12-09  
; PRIOR APPLICATION NUMBER: PCT/GB98/01681  
; PRIOR FILING DATE: 1998-06-09  
; PRIOR APPLICATION NUMBER: GB 97 11957.2  
; PRIOR FILING DATE: 1997-06-09  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: CTL Epitope of the Malaria String  
US-10-653-624-8

Query Match 100.0%; Score 42; DB 16; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
Db 3 KNKEKALII 11

## RESULT 5

US-10-833-439-8  
; Sequence 8, Application US/10833439  
; Publication No. US20040175365A1  
; GENERAL INFORMATION:

```
/ APPLICANT: McMichael, Andrew
/ APPLICANT: Hill, Adrian V.S.
/ APPLICANT: Gilbert, Sarah C.
/ APPLICANT: Schneider, Jorg
/ APPLICANT: Plebanski, Magdalena
/ APPLICANT: Hanke, Tomas
/ APPLICANT: Smith, Geoffrey L.
/ APPLICANT: Blanchard, Tom
/ TITLE OF INVENTION: Methods and Reagents for Vaccination
/ FILE REFERENCE: 2907.1000-000
/ CURRENT APPLICATION NUMBER: US/10/833,439
/ PRIOR FILING DATE: 2004-04-28
/ PRIOR FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: US/09/454,204
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: PCT/GB98/01681
/ PRIOR FILING DATE: 1998-06-09
/ PRIOR APPLICATION NUMBER: GB 97 11957.2
/ PRIOR FILING DATE: 1997-06-09
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-439-8

Query Match      100.0%; Score 42; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 KKKKALII 9
Db 3 KKKKALII 11

RESULT 6
US-10-833-745-8
/ Sequence 8, Application US/10833745
/ Publication No. US2004019127A1
/ GENERAL INFORMATION:
/ APPLICANT: McMichael, Andrew
/ APPLICANT: Hill, Adrian V.S.
/ APPLICANT: Gilbert, Sarah C.
/ APPLICANT: Schneider, Jorg
/ APPLICANT: Plebanski, Magdalena
/ APPLICANT: Hanke, Tomas
/ APPLICANT: Smith, Geoffrey L.
/ APPLICANT: Blanchard, Tom
/ TITLE OF INVENTION: Methods and Reagents for Vaccination
/ FILE REFERENCE: 2907.1000-000
/ CURRENT APPLICATION NUMBER: US/10/833,745
/ PRIOR FILING DATE: 2004-04-28
/ PRIOR FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: US/09/454,204
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: PCT/GB98/01681
/ PRIOR FILING DATE: 1998-06-09
/ PRIOR APPLICATION NUMBER: GB 97 11957.2
/ PRIOR FILING DATE: 1997-06-09
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-745-8

Query Match      100.0%; Score 42; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 KKKKALII 9
Db 3 KKKKALII 11

RESULT 7
US-10-833-744-8
/ Sequence 8, Application US/10833744
/ Publication No. US20040197349A1
/ GENERAL INFORMATION:
/ APPLICANT: McMichael, Andrew
/ APPLICANT: Hill, Adrian V.S.
/ APPLICANT: Gilbert, Sarah C.
/ APPLICANT: Schneider, Jorg
/ APPLICANT: Plebanski, Magdalena
/ APPLICANT: Hanke, Tomas
/ APPLICANT: Smith, Geoffrey L.
/ APPLICANT: Blanchard, Tom
/ TITLE OF INVENTION: Which Generate A CD8 T Cell Immune Response
/ FILE REFERENCE: 2907.1000-000
/ CURRENT APPLICATION NUMBER: US/10/833,744
/ CURRENT FILING DATE: 2004-04-08
/ PRIOR FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: US/09/454,204
/ PRIOR FILING DATE: 1999-12-09
/ PRIOR APPLICATION NUMBER: PCT/GB98/01681
/ PRIOR FILING DATE: 1998-06-09
/ PRIOR APPLICATION NUMBER: GB 97 11957.2
/ PRIOR FILING DATE: 1997-06-09
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-833-744-8

Query Match      100.0%; Score 42; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.27; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0;

QY 1 KKKKALII 9
Db 3 KKKKALII 11

RESULT 8
US-10-686-943-8
/ Sequence 8, Application US/10686943
/ Publication No. US20040213799A1
/ GENERAL INFORMATION:
/ APPLICANT: McMichael, Andrew
/ APPLICANT: Hill, Adrian V.S.
/ APPLICANT: Gilbert, Sarah C.
/ APPLICANT: Schneider, Jorg
/ APPLICANT: Plebanski, Magdalena
/ APPLICANT: Hanke, Tomas
/ APPLICANT: Smith, Geoffrey L.
/ APPLICANT: Blanchard, Tom
/ TITLE OF INVENTION: Methods and Reagents for Vaccination
/ FILE REFERENCE: 2907.1000-000
```

```

; CURRENT APPLICATION NUMBER: US/10/686,943
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: CTL Epitope of the Malaria String
US-10-686-943-8

```

```

Query Match      100.0%; Score 42; DB 17; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KNKEKALII 9
        |||||
Db      3 KNKEKALII 11

```

## RESULT 9

```

US-10-079-167-41
; Sequence 41, Application US/10079167
; Publication No. US20030138454A1
; GENERAL INFORMATION:
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: McShane, Helen
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Reece, William
; APPLICANT: Schneider, Joerg
; TITLE OF INVENTION: Vaccination Method
; FILE REFERENCE: 2907.1000-001
; CURRENT APPLICATION NUMBER: US/10/079,167
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: US 09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; PRIOR APPLICATION NUMBER: PCT/GB01/04116
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: GB 00 23203.3
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
US-10-079-167-41

```

```

Query Match      100.0%; Score 42; DB 14; Length 229;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KNKEKALII 9
        |||||
Db      58 KNKEKALII 66

```

## RESULT 10

```

US-10-653-624-41
; Sequence 41, Application US/10653624

```

```

; Publication No. US20040131594A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Joerg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/653,624
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/454,204A
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Complete Epitope of Malaria String
US-10-653-624-41

```

```

Query Match      100.0%; Score 42; DB 16; Length 229;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 KNKEKALII 9
        |||||
Db      58 KNKEKALII 66

```

## RESULT 11

```

US-10-833-439-41
; Sequence 41, Application US/10833439
; Publication No. US20040175365A1
; GENERAL INFORMATION:
; APPLICANT: McMichael, Andrew
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Schneider, Joerg
; APPLICANT: Plebanski, Magdalena
; APPLICANT: Hanke, Tomas
; APPLICANT: Smith, Geoffrey L.
; APPLICANT: Blanchard, Tom
; TITLE OF INVENTION: Methods and Reagents for Vaccination
; FILE REFERENCE: 2907.1000-000
; CURRENT APPLICATION NUMBER: US/10/833,439
; CURRENT FILING DATE: 2004-04-28
; PRIOR APPLICATION NUMBER: US/10/686,943
; PRIOR FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: US/09/454,204
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: PCT/GB98/01681
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: GB 97 11957.2
; PRIOR FILING DATE: 1997-06-09
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:

```

OTHER INFORMATION: Complete Epitope of Malaria String  
US-10-833-439-41

Query Match 100.0%; Score 42; DB 16; Length 229;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 58 KNKEKALII 66

## RESULT 12

US-10-833-745-41  
; Sequence 41, Application US/10833745  
; Publication No. US20040191272A1

## GENERAL INFORMATION:

; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg  
; APPLICANT: Plebanski, Magdalena  
; APPLICANT: Hanke, Tomas  
; APPLICANT: Smith, Geoffrey L.  
; APPLICANT: Blanchard, Tom

; TITLE OF INVENTION: Methods and Reagents for Vaccination  
; FILE REFERENCE: 2907.1000-000

; CURRENT APPLICATION NUMBER: US/10/833,745

; CURRENT FILING DATE: 2004-04-28

; PRIOR APPLICATION NUMBER: US/10/686,943

; PRIOR FILING DATE: 2003-10-16

; PRIOR APPLICATION NUMBER: US/09/454,204

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: PCT/GB98/01681

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: GB 97 11957.2

; PRIOR FILING DATE: 1997-06-09

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 41

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

OTHER INFORMATION: Complete Epitope of Malaria String

US-10-833-745-41

Query Match 100.0%; Score 42; DB 17; Length 229;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 58 KNKEKALII 66

## RESULT 13

US-10-833-744-41

; Sequence 41, Application US/10833744

; Publication No. US20040197349A1

## GENERAL INFORMATION:

; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg  
; APPLICANT: Plebanski, Magdalena  
; APPLICANT: Hanke, Tomas  
; APPLICANT: Smith, Geoffrey L.  
; APPLICANT: Blanchard, Tom

; TITLE OF INVENTION: Methods and Reagents for Vaccination

; FILE REFERENCE: 2907.1000-000

OTHER INFORMATION: Complete Epitope of Malaria String  
US-10-833-744-41

Query Match 100.0%; Score 42; DB 17; Length 229;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 58 KNKEKALII 66

US-10-833-745-41  
; Sequence 41, Application US/10686943  
; Publication No. US20040213799A1

## GENERAL INFORMATION:

; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg  
; APPLICANT: Plebanski, Magdalena  
; APPLICANT: Hanke, Tomas  
; APPLICANT: Smith, Geoffrey L.  
; APPLICANT: Blanchard, Tom

; TITLE OF INVENTION: Methods and Reagents for Vaccination  
; FILE REFERENCE: 2907.1000-000

; CURRENT APPLICATION NUMBER: US/10/833,744

; CURRENT FILING DATE: 2004-04-08

; PRIOR APPLICATION NUMBER: US/09/454,204

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: PCT/GB98/01681

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: GB 97 11957.2

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 41

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

OTHER INFORMATION: Complete Epitope of Malaria String

US-10-833-744-41

Query Match 100.0%; Score 42; DB 17; Length 229;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 58 KNKEKALII 66

US-10-833-745-41  
; Sequence 41, Application US/10686943  
; Publication No. US20040213799A1

## GENERAL INFORMATION:

; APPLICANT: McMichael, Andrew  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Schneider, Jorg  
; APPLICANT: Plebanski, Magdalena  
; APPLICANT: Hanke, Tomas  
; APPLICANT: Smith, Geoffrey L.  
; APPLICANT: Blanchard, Tom

; TITLE OF INVENTION: Methods and Reagents for Vaccination

; FILE REFERENCE: 2907.1000-000

; CURRENT APPLICATION NUMBER: US/10/686,943

; CURRENT FILING DATE: 2003-10-16

; PRIOR APPLICATION NUMBER: US/09/454,204

; PRIOR FILING DATE: 1999-12-09

; PRIOR APPLICATION NUMBER: PCT/GB98/01681

; PRIOR FILING DATE: 1998-06-09

; PRIOR APPLICATION NUMBER: GB 97 11957.2

; NUMBER OF SEQ ID NOS: 78

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 41

; LENGTH: 229

; TYPE: PRT

; ORGANISM: Unknown

; FEATURE:

OTHER INFORMATION: Complete Epitope of Malaria String

US-10-686-943-41

Query Match 100.0%; Score 42; DB 17; Length 229;  
Best Local Similarity 100.0%; Pred. No. 6;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KNKEKALII 9  
| | | | |  
Db 58 KNKEKALII 66

## RESULT 15

```

US-10-437-963-105530
; Sequence 105530, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 105530
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_102766C.1.pap
US-10-437-963-105530

Query Match          92.9%; Score 39; DB 16; Length 119;
Best Local Similarity 77.8%; Pred. No. 11;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      1 KNKEKALII 9
Db      82 KNKEKALLV 90

```

Search completed: December 6, 2004, 15:36:08  
Job time : 100 secs